

40

Access DB# 40349

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

Searcher: Chen - Joly
 Searcher Phone #: 308-4501
 Searcher Location: Biochem Lab
 Date Searcher Picked Up: 4/17/01
 Date Completed: 4/25/01
 Searcher Prep & Review Time: _____
 Clerical Prep Time: 5 min
 Online Time: 8 min

Type of Search

NA Sequence (#) 1
 AA Sequence (#) 1
 Structure (#) _____
 Bibliographic _____
 Litigation _____
 Fulltext _____
 Patent Family _____
 Other _____

Vendors and cost where applicable

STN _____
 Dialog _____
 Questel/Orbit _____
 Dr. Link _____
 Lexis/Nexis _____
 Sequence Systems ABS502/Compugen 1
 WWW/Internet _____
 Other (specify) _____

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STIC-Biotech/ChemLib

40344

From: Chan, Christina
Sent: Tuesday, April 17, 2001 12:05 PM
To: Kemmerer, Elizabeth; STIC-Biotech/ChemLib
Subject: RE: rush seq search req

[Handwritten signature]

~~Please rush.~~ **Thanks Chris**

Chris Chan
TC 1600 New Hire Training Coordinator and SPE, 1644
CM 1, Room 9B19
308-3973

CRFE

-----Original Message-----

From: **Kemmerer, Elizabeth**
Sent: Tuesday, April 17, 2001 12:05 PM
To: Chan, Christina
Subject: rush seq search req

Hi, Christina-
Please approve the following for an overdue amended from Garnette Draper's docket. Thanks!

STIC:
Please rush a regular + interference search of SEQ ID NOS: 25 and 26 for 08/741095. Thanks,

Elizabeth (Betsy) Kemmerer
Art Unit 1646
308-2673
CM1-10B17

This search was run on the machines we identify as Compugen1, abss03, abss04, or abss05. The databases on these machines are exactly the same as those on the other machines. However, for searches run on the listed machines, two sets of results are now generated when the Pending Nucleic Acid and/or Pending Amino Acid databases are searched. The Pending databases have been split into two parts to reduce the amount of time required for their daily update.

Searches run against the Nucleic Acid Pending database will produce two sets of results, with the extensions **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database will produce two sets of results, with the extensions **.rapm** and **.rapn**

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 24, 2001, 14:12:42 ; Search time 71.66 seconds

(without alignments)
4618.460 Million cell updates/sec

Title: US-08-741-095B-25

Perfect score: 881

Sequence: 1 cctgagcagatgagcctcct.....ccacagactgcaccccca 881

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_36.*

- 1: /cgnl_8/gcgdata/geneseq/geneseqn/NA1980.DAT.*
- 2: /cgnl_8/gcgdata/geneseq/geneseqn/NA1981.DAT.*
- 3: /cgnl_8/gcgdata/geneseq/geneseqn/NA1982.DAT.*
- 4: /cgnl_8/gcgdata/geneseq/geneseqn/NA1983.DAT.*
- 5: /cgnl_8/gcgdata/geneseq/geneseqn/NA1984.DAT.*
- 6: /cgnl_8/gcgdata/geneseq/geneseqn/NA1985.DAT.*
- 7: /cgnl_8/gcgdata/geneseq/geneseqn/NA1986.DAT.*
- 8: /cgnl_8/gcgdata/geneseq/geneseqn/NA1987.DAT.*
- 9: /cgnl_8/gcgdata/geneseq/geneseqn/NA1988.DAT.*
- 10: /cgnl_8/gcgdata/geneseq/geneseqn/NA1989.DAT.*
- 11: /cgnl_8/gcgdata/geneseq/geneseqn/NA1990.DAT.*
- 12: /cgnl_8/gcgdata/geneseq/geneseqn/NA1991.DAT.*
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- 19: /cgnl_8/gcgdata/geneseq/geneseqn/NA1998.DAT.*
- 20: /cgnl_8/gcgdata/geneseq/geneseqn/NA1999.DAT.*
- 21: /cgnl_8/gcgdata/geneseq/geneseqn/NA2000.DAT.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	881	100.0	881	17 T40048	Human tumour necro
2	879.4	99.8	1704	19 V4509	Human TNF receptor
3	879.4	99.8	1704	20 V83763	Human tumour necro
4	873	99.1	1724	18 T51737	Human hepes slmpt
5	873	99.1	1724	20 X25512	Hepes virus entry
6	858.4	97.4	927	19 V44852	Hepesvirus encodn
7	858.4	97.4	927	20 X87265	CDNA clone encodn
8	732.4	83.1	1834	21 Z94198	Membrane-bound her
9	688.8	78.2	1929	21 Z94195	Soluble herpesvitu
10	671.4	76.2	1596	21 Z94196	Soluble herpesvitu
11	555.8	63.1	2313	21 Z94197	Soluble herpesvitu
12	342.2	38.8	2692	19 V34510	Human TNF receptor

13	306.2	34.8	723	17 T40049	Human tumour necro
14	239.4	27.2	2637	19 V43511	Human TNF receptor
15	233.4	26.5	405	17 T40050	Human tumour necro
16	62	7.0	2393	12 O10907	40KD TNF inhibitor
17	60.4	6.9	705	19 V41549	Human soluble tumo
18	60.4	6.9	705	19 V19802	Tumour necrosis fa
19	60.4	6.9	705	20 V81733	Tumour necrosis in
20	59.6	6.8	1691	16 T05443	BamPp delta53 nerv
21	58.6	6.7	1004	13 O21176	Human CD40 antigen
22	58.6	6.7	1004	14 O47341	CD40 coding sequen
23	58	6.6	705	21 Z45760	DNA encoding a K12
24	58	6.6	705	21 Z45762	Wild type N-termina
25	58	6.6	1557	15 Q45225	Sequence encoding
26	58	6.6	1640	12 O10990	Partial sequence o
27	58	6.6	1641	14 O49931	TNF-R CDNA. Homo
28	58	6.6	2224	16 O89544	p75 Tumour Necrosi
29	57	6.5	822	21 Z55527	Canine CD40 CDNA c
30	57	6.5	822	21 Z55528	Canine CD40 CDNA c
31	57	6.5	1004	17 N90617	CD40 CDNA. N9061
32	57	6.5	1004	17 T14706	Human CD40 antigen
33	57	6.5	1004	19 V63454	Human CD40 antigen
34	57	6.5	1004	20 Z23432	Human CD40 DNA. H
35	57	6.5	1004	20 Z40936	Human CD40 encodin
36	57	6.5	1004	20 V81198	Human CD40 antigen
37	57	6.5	1004	21 Z47769	Human CD40 nucleot
38	57	6.5	1425	21 Z55525	Canine CD40 CDNA.
39	57	6.5	1425	21 Z55526	Canine CD40 CDNA c
40	56.4	6.4	705	21 Z45759	DNA encoding a K10
41	56.4	6.4	705	21 Z45761	DNA encoding a K10
42	55.4	6.3	1004	20 Z20296	CD40 CDNA. Unden
43	51	5.8	765	21 Z55529	Canine mature CD40
44	51	5.8	765	21 Z55530	Canine mature CD40
45	50.8	5.8	1641	15 Q45224	Sequence encoding

ALIGNMENTS

RESULT 1	
T40048	
ID T40048 standard; cDNA: 881 BP.	
XX	
AC T40048;	
XX	
DT 30-JUN-1997 (first entry)	
XX	
DE Human tumour necrosis factor receptor cDNA.	
XX	
KW Human; tumour necrosis factor; TNF; receptor; treatment;	
KW activation; inhibition; identification; agonist; antagonist;	
KW stimulation; T cell; differentiation; mediation; immune;	
KW antiviral; response; regulation; growth; protection; HIV;	
KW radiation; Chlamydia; infection; immunodeficiency; virus;	
KW autoimmune disease; inflammation; septic shock; cerebral;	
KW cachexia; B cell; cancer; graft; host; reaction; rejection;	
KW prevention; apoptosis; cytotoxicity; hybridisation probe;	
XX detection; antibody; reagent; ss.	
XX	
OS Homo sapiens.	
XX	
FH Key	Location/Qualifiers
FT CDS	9..860
FT	/*tag= a
FT	sig_peptide
FT	9..122
FT	/*tag= b
FT	mat_peptide
FT	123..857
FT	/*tag= c
PN	/product= tumour_necrosis_factor_receptor
XX	
XX	W09634095-A1.
XX	
PD	31-OCT-1996.
XX	

27-APR-1995; 95MO-US050508.
27-APR-1995; 95MO-US050508.
(HUMA-) HUMAN GENOME SCI INC.
Gentz R, NI J, Rosen CA;
WPI: 1996-497627/49.
P-PSDB; W05809.
New nucleic acid encoding a human tumour necrosis factor receptor -
useful for treatment of auto-immune diseases etc., in diagnosis and
for drug screening
Claim 10; Page 47; 73pp; English.

[illegible]

Db	481	aggaaacccctgtgtcagagacgtgcccccgcgggagaccttctctccaatgaggacccttgagg	540
Oy	541	aatgtcagaccacagaccaaagtgcagcgtgtgctgtgtgacgaagcccgagcctgtggacacga	600
Db	541	aatgtcagaccacagaccaaagtgcagcgtgtgctgtgtgacgaagcccgagcctgtggacacga	600
Oy	601	gtcccaactgggtgtgtgtgtgttctctcagaggagccctcgtcactgcatgtgtgtgtccca	660
Db	601	gtcccaactgggtgtgtgtgtgttctctcagaggagccctcgtcactgcatgtgtgtgtccca	660
Oy	661	cagttgtgcctaatatattgtgtgaaaaagaaagacaaaggggtgtatgtagtcaaggtga	720
Db	661	cagttgtgcctaatatattgtgtgaaaaagaaagacaaaggggtgtatgtagtcaaggtga	720
Oy	721	tcgtctccgtccagtcgagaaagacagagtgagaaggltgagggccacagtcattgtgagccc	780
Db	721	tcgtctccgtccagtcgagaaagacagagtgagaaggltgagggccacagtcattgtgagccc	780
Oy	761	tgcagagccctcccgagcgtacacacggtgtgscgtgtgagggagaatactcctcatltaagg	840
Db	761	tgcagagccctcccgagcgtacacacggtgtgscgtgtgagggagaatactcctcatltaagg	840
Oy	841	ggagagaccacaacacactgacccacagactctgaccccga	881
Db	841	ggagagaccacaacacactgacccacagactctgaccccga	881
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ID	V34509	standard; cDNA; 1704 bp.	
XX	XX	V34509;	
AC	XX		
XX	XX		
DT	25-SEP-1998	(first entry)	
XX	XX		
DE	Human TNF receptor related (TR2) gene.		
XX	XX		
KM	ds; human; tumour necrosis factor; TNF; herpes simplex virus;		
KW	aberrant cell survival; radiation therapy; lymphocyte proliferation;		
KM	immune deficiency syndrome.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
FH	Key	Location/Qualifiers	
FT	CDS	265..1116	
FT		/*tag= a	
FT		/product= "TR2 protein"	
FT	sig_peptide	265..372	
FT		/*tag= b	
FT	mat_peptide	373..1116	
FT		/*tag= c	
XX	XX		
PN	WO9818824-A1.		
XX	XX		
PD	07-MAY-1998.		
XX	XX		
PE	30-OCT-1996;	96WO-US18540.	
XX	XX		
PR	30-OCT-1996;	96WO-US18540.	
XX	XX		
PA	(HUMA-) HUMAN GENOME SCI INC.		
PA	(SMIK) SMITHKLINE BEECHAM CORP.		
PI	Genztz RL, Hurlle MR, Lyn SDP, Ni J, Rosen CA;		
XX	XX		
DR	WPI: 1998-272139/24.		
DR	P-PSDB; W460045.		
XX	XX		
PT	Nucleic acid encoding TR2 tumour necrosis factor family receptor -		
PT	and its splice variants, useful for diagnosis and treatment of		
PT	diseases involving abnormal cell survival or death, e.g. herpes		
PT	simplex infection		
XX	XX		

XX	RESULT	2
XX	V34509	
ID	V34509	standard; CDNA; 1704 BP.
XX	XX	
AC	V34509;	
XX	XX	
DT	25-SEP-1998	(first entry)
XX	XX	
DE	Human TNF receptor related	(TR2) gene.
XX	XX	
KW	ds: human: tumour necrosis factor; TNF; herpes simplex virus;	
KW	aberrant cell survival; radiation therapy; lymphocyte proliferative	
KW	immune deficiency syndrome.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
FH	Key	Location/Qualifiers
FT	CDS	265..1116
FT		/*tag= a
FT		/product= "TR2 protein"
FT	sig_peptide	265..372
FT		/*tag= b
FT	mat_peptide	373..1116
FT		/*tag= c
XX	XX	
PN	W09818824 -A1.	
XX	XX	
PD	07-MAY-1998.	
XX	XX	
PF	30-OCT-1996;	96WO-US18540.
XX	XX	
PR	30-OCT-1996;	96WO-US18540.
XX	XX	
PA	(HUMA-) HUMAN GENOME SCI INC.	
PA	(SMIR) SMITHKLINE BEECHAM CORP.	
XX	XX	
PI	Gentz RL, Hurle MR, Lyn SDP, Ni J, Rosen CA;	
DR	WPI: 1998-272139/24.	
DR	P-PSDB: W460045.	
XX	XX	
PT	Nucleic acid encoding TR2 tumour necrosis factor family receptor	
PT	and its splice variants; useful for diagnosis and treatment of	
PT	diseases involving abnormal cell survival or death, e.g. herpes	
XX	simplex infection	
XX	XX	

PS Claim 2; p86-88; 151pp; English.

CC The human tumour necrosis factor (TNF) receptor related protein (TR2) is
 CC a member of the TNF family and displays considerable homology to murine
 CC CD40. It can be used in soluble forms to treat herpes simplex virus
 CC infection and TR2 proteins (or their agonists or antagonists) are used to
 CC treat disease associated with aberrant cell survival. Agonists may also
 CC be used to protect against the effects of radiation therapy and to
 CC stimulate lymphocyte proliferation and differentiation in patients
 CC infected by human immune deficiency syndrome.

XX Sequence 1704 BP; 343 A; 529 C; 504 G; 328 T; 0 other:

Query Match 99.8%; Score 879.4; DB 19; Length 1704;
 Best Local Similarity 99.9%; Pred. No. 4.3e-214;
 Matches 880; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 cctgaagcatgagagcctctcgtgagactgaggcctcctcctctgagatccacccacgaa 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 257 cctgaagcatgagagcctcctcgtgagactgaggcctcctcctcctgagatccacccacgaa 316

QY 61 ccgagcgtcttgagagctgctgctgctatctcaactctcctgaggagccctctgtagcccg 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 317 ccgagcgtcttgagagctgctgctgctatctcaactctcctgaggagccctctgtagcccg 376

QY 121 cctgcgcctctcctgaag 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 377 cctgcgcctctcctgaag 436

QY 181 gtcacagttatcgtgtgaaagagagagagagagagagagagagagagagagagagag 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 437 gtcacagttatcgtgtgaaagagagagagagagagagagagagagagagagagagag 496

QY 241 gccctcag 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 497 gccctcag 556

QY 301 tgtgtgacccag 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 557 tgtgtgacccag 616

QY 361 tgtgtgacccag 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 617 tgtgtgacccag 676

QY 421 gccgcgtctcag 480
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 DB 677 gccgcgtctcag 736

QY 481 aggacacccgtgtcagaactgcccccgaggagcctctctccaaatggagacctgagag 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 737 aggacacccgtgtcagaactgcccccgaggagcctctctccaaatggagacctgagag 796

QY 541 aatgtcagacacag 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 797 aatgtcagacacag 856

QY 601 gctccacagtggtatggtgttctctcagagagagagagagagagagagagagagagag 660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 857 gctccacagtggtatggtgttctctcagagagagagagagagagagagagagagagag 916

QY 661 cagttgagcctaatacatgtgtgtaaaagagagagagagagagagagagagagagagag 720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 917 cagttgagcctaatacatgtgtgtaaaagagagagagagagagagagagagagagagag 976

QY 721 tctgtctcgtcagcagcagaaagagagagagagagagagagagagagagagagagagag 780
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 781 tgcagagcctcctcag 840
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1037 tgcagagcctcctcag 1096

QY 841 ggaagagcccaactgacccacagactctgacccga 881
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1097 ggaagagcccaactgacccacagactctgacccga 1137

RESULT 3
 ID V83763
 DB V83763 standard; cDNA; 1704 BP.

AC V83763;

DT 17-MAR-1999 (first entry)

DE Human tumour necrosis factor receptor-like 2 protein coding sequence.

DE Tumour necrosis factor receptor-like 2; TR2; TNF; human; psoriasis;

KW systemic lupus erythematosus; idiopathic thrombocytopenic purpura;

KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;

KW insulin-dependent diabetes mellitus; allergic disorder; cancer; therapy;

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 265..1116

FT /tag- a

PN WO9851346-A1.

PD 19-NOV-1998.

PF 12-MAY-1998; 98MO-US09744.

PR 12-MAY-1997; 97US-0046249.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PI (SMIK) SMITHKLINE BEECHAM PLC.

PI Harrop JA, Holmes SD, Reddy MP, Truneh A;

DR MPI; 1999-059689/05.

DR P-PSDB; W87591.

PT Method of treating pathological condition - comprises administering

PT tumour necrosis factor-2 antibody to patient

PS Disclosure; Page 26-27; 35pp; English.

CC This sequence encodes the human tumour necrosis factor (TNF)

CC receptor-like 2 (TR2) protein. Antibodies that target the TR2 protein can

CC be used in the method of the invention to treat pathological conditions.

CC The method is used to treat systemic lupus erythematosus, idiopathic

CC thrombocytopenic purpura, rheumatoid arthritis, multiple sclerosis,

CC psoriasis, inflammatory bowel disease, insulin-dependent diabetes

CC mellitus, allergic disorders, e.g. asthma, allergic rhinitis and atopic

CC dermatitis, cancer, e.g. lymphomas and leukaemias, atherosclerosis and

CC viral infections, e.g. Herpes simplex virus and AIDS. The TR2 antibody

CC is also used to monitor and diagnose abnormalities in TR-2 function,

CC production or metabolism.

SO Sequence 1704 BP; 343 A; 529 C; 504 G; 328 T; 0 other:

Query Match 99.8%; Score 879.4; DB 20; Length 1704;
 Best Local Similarity 99.9%; Pred. No. 4.3e-214;
 Matches 880; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 cctgaagcatgagagcctcctcgtgagactgaggcctcctcctctgagatccacccacgaa 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 257 cctgaagcatgagagcctcctcgtgagactgaggcctcctcctcctgagatccacccacgaa 316

QY 61 ccgagcgtcttgagagctgctgctgctatctcaactctcctgaggagccctctgtagcccg 120

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Db 317 cccagctcttgagcgtgctgtatctcaacctctctggagagccctctgaagcccccag 376
QY 121 ctctgcgtctctgcaagagagacagtaaccagtggtctccagatgctgcacaaagtga 180
Db 377 ctctgcgtctctgcaagagagacagtaaccagtggtctccagatgctgcacaaagtga 436
QY 181 gtccaggtatctgtgaaagagagcctgagggagagctgagggagagagagtgtaacct 240
Db 437 gtccaggtatctgtgaaagagagcctgagggagagctgagggagagagtgtaacct 496
QY 241 gccctcagagacactatctgcccacactcaatgacctgaagcaagtcttgcagtccaa 300
Db 497 gccctcagagacactatctgcccacactcaatgacctgaagcaagtcttgcagtccaa 556
QY 301 tctgtgacccagcactgagcctgagcgagagccggaactgctccagagacagagacgcg 360
Db 557 tctgtgacccagcactgagcctgagcgagagccggaactgctccagagacagagacgcg 616
QY 361 tctgtggttgagccagagcacttctgcatctgacagagagagagacagcgcgcgt 420
Db 617 tctgtggttgagccagagcacttctgcatctgacagagagagagacagcgcgcgt 676
QY 421 gccgcgtctacgacacactccagcccgagagaggtgacagagagagagagagagagtc 480
Db 677 gccgcgtctacgacacactccagcccgagagaggtgacagagagagagagagagagtc 736
QY 481 agagacacactgtgtcagaactgcccccgaggagccttctcccaatggagccttgagg 540
Db 737 agagacacactgtgtcagaactgcccccgaggagccttctcccaatggagccttgagg 796
QY 541 aatgtacagcaccagacagatgagctgctgtgtgacagagagcgcgagctggagacagca 600
Db 797 aatgtacagcaccagacagatgagctgctgtgtgacagagagcgcgagctggagacagca 856
QY 601 gctccacactggtatgtgtgttctctcagagagcctcgtcatgcatgtttgtctcca 660
Db 857 gctccacactggtatgtgtgttctctcagagagcctcgtcatgcatgtttgtctcca 916
QY 661 cagttggtctaatcatatgtgtgaaagagagagagagagagagagagagagagagag 720
Db 917 cagttggtctaatcatatgtgtgaaagagagagagagagagagagagagagagagag 976
QY 721 tctgtcctctcagcgagaaagacagagagagagagagagagagagagagagagagagag 780
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QY 781 tgcagagccctccgagagcgtacacagctgagcggtgagagagagagagagagagagag 840
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QY 841 gagagagagagagagagagagagagagagagagagagagagagagagagagagagag 881
Db 1097 gagagagagagagagagagagagagagagagagagagagagagagagagagagagag 1137

RESULT 4
T51737
ID T51737 standard; cDNA: 1724 BP.
XX
AC T51737;
XX
DT 07-MAY-1997 (first entry)
XX
DE Human herpes simplex virus cellular mediator cDNA.
XX
KW Herpes simplex virus cellular mediator; HVEM; receptor; HSV;
XX
OS diagnosis; therapy; antisense; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 294..1145

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FT FT sig_peptide /tag= a
FT FT mat_peptide /tag= b
FT FT /tag= c
FT FT /note= "the mature protein coding sequence is preferred for use in constructs of the invention"
FT FT
PN W09704658-A1.
XX
PD 13-FEB-1997.
XX
PF 26-JUL-1996; 96WO-US12374.
XX
PR 28-JUL-1995; 95US-0509024.
XX
PA (NOUN ) UNITV NORTHWESTERN.
XX
PI Montgomery RI, Spear PG;
XX
PI MPI: 1997-145273/13.
XX
DR P-PSDB; W12659.
XX
XX New human herpes simplex virus cellular mediator - used for
XX PT diagnosis, drug screening and therapeutically to inhibit entry of
XX PT HSV into cells
XX
PS Claim 4; Page 37-38; 54pp; English.
XX
CC A cDNA insert (T51737) in plasmid pBEC580 codes for human herpes
CC CC simplex virus (HSV) cellular mediator (HVEM) (W12659), a novel
CC CC member of the TNF/NGF receptor family that mediates or enhances
CC CC entry of HSV into cells. It was isolated by screening a HeLa cDNA
CC CC expression library for genes capable of converting CHO-K1 cells
CC CC from resistance to susceptibility to HSV-1 entry. The clone can be
CC CC used to produce recombinant HVEM in host (esp. CHO) cells. Sense
CC CC oligonucleotides based on the sequence can be used as probes or
CC CC primers for identifying related sequences, while antisense
CC CC sequences can be used therapeutically to prevent HSV entry into
CC CC cells.
XX
SQ Sequence 1724 BP; 331 A; 548 C; 512 G; 333 T; 0 other;

Query Match 99.1%; Score 873; DB 18; Length 1724;
Best Local Similarity 99.4%; Pred. No. 1.8e-212;
Matches 876; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 cctgagagatgagcctcctgagagactgggggctcctcctctgagagatcacccacagaa 60
Db 286 cctgagagatgagcctcctgagagactgggggctcctcctcctgagagatcacccacagaa 345
QY 61 ccgagccttgagagctgtgtgtatctcaacctctcctggagagccctgtcagccag 120
Db 346 ccgagccttgagagctgtgtgtatctcaacctctcctggagagccctgtcagccag 405
QY 121 ctctgcgtctcctgagagagagagagagagagagagagagagagagagagagagagagag 180
Db 406 ctctgcgtctcctgagagagagagagagagagagagagagagagagagagagagagagag 465
QY 181 gtccaggtatctgtgaaagagagcctgagggagagctgacagagagagagagagagagag 240
Db 466 gtccaggtatctgtgaaagagagcctgagggagagctgacagagagagagagagagagag 525
QY 241 gccctcagagacactatctgcccacactcaatgacctgaagcaagtgtctgcagtgccaa 300
Db 526 gccctcagagacactatctgcccacactcaatgacctgaagcaagtgtctgcagtgccaa 585
QY 301 tctgtgacccagcactgagcctgagcgagagccggaactgctccagagagagagagagag 360
Db 586 tctgtgacccagcactgagcctgagcgagagccggaactgctccagagagagagagagag 645

```

QY 361 tttgtgttgagcccaagccactctctgcatcgtccaggaagggagccactgcccgcgt 420
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 QY 421 gccgagctaacgcccaccccgagcccgaggggtgcagaaaggagcccgagatc 480
 Db 706 gccgcgttaagccaccccccagcccgagggggtgcagaaaggagcccgagatc 765
 QY 481 aggaacacctgtgtcagaactgcccccgaggagactctctcccaatlggaaccttgagg 540
 Db 766 aggaacacctgtgtcagaactgcccccgaggagactctctcccaatlggaaccttgagg 825
 QY 541 aatgtcagaccagaccagcaagtgcagctgctgtgcaagaaagccggagcttggaacca 600
 Db 826 aatgtcagaccagaccagcaagtgcagctgctgtgcaagaaagccggagcttggaacca 885
 QY 601 gctccactgggtatgtgtgtctctcagaggagctctgcatcgtctgtttgtccca 660
 Db 886 gctccactgggtatgtgtgtctctcagaggagctctgcatcgtctgtttgtccca 945
 QY 661 cagttgacctaatcatatgtgtgaaagaagcaaggggtgattgatacagatga 720
 Db 946 cagttgacctaatcatatgtgtgaaagaagcaaggggtgattgatacagatga 1005
 QY 721 tctgtccgtccagcggaagaaagacagagagagagtgagagccagtcataagagcc 780
 Db 1006 tctgtccgtccagcggaagaaagacagagagagagtgagagccagtcataagagcc 1065
 QY 781 tgcagggccctccgagctcagccaggtggtgagggagacaatccccctaccag 840
 Db 1066 tgcagggccctccgagctcagccaggtggtgagggagacaatccccctaccag 1125
 QY 841 ggaagagcccaaacactgacccacagactctgaccccca 881
 Db 1126 ggaagagcccaaacactgacccacagactctgaccccca 1166
 RESULT 5
 X25512
 ID X25512 standard; cDNA. 1724 BP.
 AC X25512;
 XX
 DT 02-AUG-1999 (first entry)
 XX
 DE Herpes virus entry mediator (HVEM) cDNA.
 XX
 KW Herpes virus entry mediator; HVEM; HSV receptor; infection;
 KW diagnosis; therapy; vaccine; antiviral; assay; ds.
 XX
 OS Human herpes simplex virus.
 XX
 FT Key Location/Qualifiers
 FT CDS 294..1145
 FT /*tag= a
 XX
 MO9920761-A2.
 XX
 PD 29-APR-1999.
 XX
 PF 22-OCT-1998; 98WO-US22342.
 XX
 PR 22-OCT-1997; 97US-0955531.
 XX
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Fuller AO, Li Q, McLaren NC, Perez A, Subramanian G;
 XX
 DR WPI: 1999-302740/25.
 DR P-PSDB; Y05797.
 XX
 PT Human herpes simplex virus receptor B5 and HVEM compositions
 XX

PS Claim 12; Page 70-71; 89pp; English.
 XX
 CC This is the nucleotide sequence of HVEM (see Y05797), a novel
 CC human herpes simplex virus (HSV) entry mediator that is a member
 CC of the tumour necrosis factor receptor family. HVEM cDNA was
 CC isolated from a HeLa cell cDNA library on the basis of its
 CC ability to transfer HSV susceptibility to CHO cells. In the
 CC present invention, the combination of a novel porcine cell model
 CC system which is refractory to HCV entry, along with specific HSV
 CC B5 (see Y05796) and/or HVEM receptor proteins enables the
 CC development of assays for screening antiviral compounds and
 CC therapeutics. The assays are useful for detecting the ability of
 CC agents to inhibit HSV entry or spread and provide for facile
 CC high-throughput screening of compounds suspected to be able to
 CC inhibit such entry, e.g. compound libraries, peptide libraries
 CC etc., to identify potential drug candidates. The invention also
 CC provides a vaccine comprising the HSV receptor, an immunogenic
 CC polypeptide or fragments of the polypeptide.
 XX
 SQ Sequence 1724 BP; 331 A; 548 C; 512 G; 333 T; 0 other;
 Query Match 99.1%; Score 873; DB 20; Length 1724;
 Best Local Similarity 99.4%; Pred. No. 1,8e-212;
 Matches 876; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 ccttaagcatgagagccctcctggaactgggggacctctccctggagatccaccaccagaa 60
 Db 286 ccttaagcatgagagccctcctggaactgggggacctctccctggagatccaccaccagaa 345
 QY 61 ccgagctcttgaagctgtgtctgtatctcaactctctggaagccctgtctacgcccag 120
 Db 346 ccgagctcttgaagctgtgtctgtatctcaactctctggaagccctgtctacgcccag 405
 QY 121 ctctgcgcgtctctgaagaagagagagtaaccagtggctctcagtggtgtgtcccaatgca 180
 Db 406 ctctgcgcgtctctgaagaagagagagtaaccagtggctctcagtggtgtgtcccaatgca 465
 QY 181 gtccaggttactgtgtgaagagagccctgcgagggagctgacggcgacagtggtgaacct 240
 Db 466 gtccaggttactgtgtgaagagagccctgcgagggagctgacggcgacagtggtgaacct 525
 QY 241 gccctcaggacactaatctgcccactcaatgctcctaagaagtgctgtcagtgccaaa 300
 Db 526 gccctcaggacactaatctgcccactcaatgctcctaagaagtgctgtcagtgccaaa 585
 QY 301 tttgtgacccagccatggtgctgcgagccgagacgtctccaggaagagacgcgcg 360
 Db 586 tttgtgacccagccatggtgctgcgagccgagacgtctccaggaagagacgcgcg 645
 QY 361 tttgtgttgagcccaagccactctcgtatcagggcgaggccactgtgcccgcgt 420
 Db 646 tttgtgttgagcccaagccactctcgtatcagggcgaggccactgtgcccgcgt 705
 QY 421 gccgcgttaagccaccccccagcccgaggggtgcagaaaggagcccgagatc 480
 Db 706 gccgcgttaagccaccccccagcccgaggggtgcagaaaggagcccgagatc 765
 QY 481 aggaacacctgtgtcagaactgcccccgaggagactctctcccaatlggaaccttgagg 540
 Db 766 aggaacacctgtgtcagaactgcccccgaggagactctctcccaatlggaaccttgagg 825
 QY 541 aatgtcagaccagaccagcaagtgcagctgctgtgcaagaaagccggagcttggaacca 600
 Db 826 aatgtcagaccagaccagcaagtgcagctgctgtgcaagaaagccggagcttggaacca 885
 QY 601 gctccactgggtatgtgtgtctctcagaggagctctgcatcgtctgtttgtccca 660
 Db 886 gctccactgggtatgtgtgtctctcagaggagctctgcatcgtctgtttgtccca 945
 QY 661 cagttgacctaatcatatgtgtgaaagaagcaaggggtgattgatacagatga 720
 Db 946 cagttgacctaatcatatgtgtgaaagaagcaaggggtgattgatacagatga 1005

QY 721 tgcgtccgtccagcgagaaagacagagagcagaggtgagggccacagtcattgagccc 780
 CC |
 CC |
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 Db 1006 tccgtccgtccagcgagaaagacagagagcagaggtgagggccacagtcattgagccc 1065
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 CC |
 CC |
 QY 781 tgaagcgccctccgagcgtccacacagctggtccgtgagagagacaatccctcattcagcg 840
 CC |
 CC |
 CC |
 Db 1066 tgaagcgccctccgagcgtccacacagctggtccgtgagagagacaatccctcattcagcg 1125
 CC |
 CC |
 CC |
 QY 841 ggaagagagcccaaacacactgacccacagactctgcaccccgca 881
 CC |
 CC |
 CC |
 Db 1126 ggaagagagcccaaacacactgacccacagactctgcaccccgca 1166
 CC |
 CC |
 CC |
 RESULT 6
 V44852
 ID V44852 standard; DNA; 927 BP.
 AC V44852;
 XX
 XX
 DT 21-OCT-1998 (first entry)
 DE Herpesvirus entry mediator gene.
 XX
 XX Entry mediator gene; herpesvirus; HVM; tumour necrosis factor receptor;
 KM gene expression regulator; cellular stress; inflammatory response;
 KW lymphocyte activity regulator; autoimmune response; ds.
 XX
 OS Herpesvirus.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 76..927
 FT /tag= a
 FT /product= HVM
 XX
 XX W09825967-A1.
 PN 18-JUN-1998.
 PD
 XX
 XX 05-DEC-1997; 97WO-US22278.
 PF
 XX
 PR 12-DEC-1996; 96US-0032705.
 PA
 XX (GENETH) GENENTECH INC.
 PI Ashkenazi AJ, Marsters SA;
 XX
 XX WPI; 1998-348457/30.
 DR P-PSDB; W69238.
 PT
 PT Herpesvirus entry mediator polypeptide, HVM - useful, e.g. in
 PT assays for HVM and to produce antibodies and transgenic animals,
 PT e.g. for drug screening
 XX
 XX
 PS Example 1; Fig 1; 46p; English.
 XX
 CC This sequence encodes the herpesvirus entry mediator (HVM) protein of
 CC the invention. The protein is useful in quantitative diagnostic assays
 CC for HVM, in affinity purification of HVM from recombinant cells/natural
 CC sources and in competitive-type receptor binding assays. It can also be
 CC used to generate antibodies, also useful in diagnostic assays for HVM
 CC and affinity purification of HVM. HVM is believed to be a member of the
 CC tumour necrosis factor receptor (TNFR) family, and transient transfection
 CC of HVM into human 293 cells caused marked activation of certain
 CC transcription factors, e.g. Ap-1, suggesting that HVM is involved in
 CC regulating gene expression in response to infectious stimuli and cellular
 CC stresses. The predominant expression of HVM mRNA in lymphocyte-rich
 CC tissues (e.g. spleen and peripheral blood) also suggested it may be a
 CC receptor in regulating lymphocyte activity. Antibodies produced may be
 CC therefore be useful therapeutically, e.g. antagonistic antibodies may be
 CC useful to block excessive inflammatory/autoimmune response resulting from
 CC e.g. Ap-1 induction, whilst agonistic antibodies may enhance HVM
 CC regulation of such induction. The DNA may be used diagnostically, e.g.

CC to determine if DNA and/or RNA encoding HVM is present in cells, and to
 CC prepare HVM polypeptide recombinantly. It is also useful to produce
 CC non-human transgenic animals (e.g. mice or rats), especially knockout
 CC animals containing cells with an altered gene encoding HVM polypeptide.
 CC Such animals are useful in the development and screening of
 CC therapeutically useful reagents.
 XX
 XX
 SO Sequence 927 BP; 185 A; 286 C; 291 G; 165 T; 0 other;
 Query Match 97.4%; Score 856.4; DB 19; Length 927;
 Best Local Similarity 99.9%; Pred. No. 7.6e-209;
 Matches 859; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 cctgaagcattgagcgtctcctgagagctggggcgtctcctccttgagatccacccagaa 60
 Db 68 cctgaagcattgagcgtctcctgagagctggggcgtctcctccttgagatccacccagaa 127
 QY 61 ccgagctcttgaagctgtgtgtatctcaccctccttgaggccctgtctacgcccag 120
 Db 128 ccgagctcttgaagctgtgtgtatctcaccctccttgaggccctgtctacgcccag 187
 QY 121 ctctgcgtctcgaagagagacagatccacagtggtgtccgagtgctgtcccaagtga 180
 Db 188 ctctgcgtctcgaagagagacagatccacagtggtgtccgagtgctgtcccaagtga 247
 QY 181 gtccaggtatctgtgaaagagcgtctggagagctgcgagcagagatgtgtgaacct 240
 Db 248 gtccaggtatctgtgaaagagcgtctggagagctgcgagcagagatgtgtgaacct 307
 QY 241 gccctccagacactacatctgcccacactcaatgaccttaagcaagtgtctcagtgccaa 300
 Db 308 gccctccagacactacatctgcccacactcaatgaccttaagcaagtgtctcagtgccaa 367
 QY 301 tgtgtaccacagcctatggtgctgcgagcgtccgagacactgtctcagaagagaaacgcg 360
 Db 368 tgtgtaccacagcctatggtgctgcgagcgtccgagacactgtctcagaagagaaacgcg 427
 QY 361 tgtgtgttgacagccacagacactctgtgacgtccagagacgagacactgtgcgcgt 420
 Db 428 tgtgtgttgacagccacagacactctgtgacgtccagagacgagacactgtgcgcgt 487
 QY 421 gccgcgttacgacacactccagcccgagccagaggtgtcagaagagagacacagagatc 480
 Db 488 gccgcgttacgacacactccagcccgagccagaggtgtcagaagagagacacagagatc 547
 QY 481 aggaacacctgtgtcagaactgtcccccggagacactctctcccaatggaaccttgaag 540
 Db 548 aggaacacctgtgtcagaactgtcccccggagacactctctcccaatggaaccttgaag 607
 QY 541 aatgtacagcacagacaaagtgcagctgtgtgtgacgaaggtccgagctgtgagacagca 600
 Db 608 aatgtacagcacagacaaagtgcagctgtgtgtgacgaaggtccgagctgtgagacagca 667
 QY 601 gtcctcactgtgtgtgttctctcagggagacctgtcatalgtcatgtttgttcca 660
 Db 668 gtcctcactgtgtgtgttctctcagggagacctgtcatalgtcatgtttgttcca 727
 QY 661 cagtgtgctaatcatatgtgtgaaagaagaagccaaaggggtgtgtatgaatgaagtga 720
 Db 728 cagtgtgctaatcatatgtgtgaaagaagaagccaaaggggtgtgtatgaatgaagtga 787
 QY 721 tgcgtccgtccagcgagaaagacagagagcagaggtgagggccacagtcattgagccc 780
 Db 788 tgcgtccgtccagcgagaaagacagagagcagaggtgagggccacagtcattgagccc 847
 QY 781 tgaagcgccctccgagcgtccacacagctggtccgtgagagagacaatccctcattcagcg 840
 Db 848 tgaagcgccctccgagcgtccacacagctggtccgtgagagagacaatccctcattcagcg 907
 QY 841 ggaagagcccaaacacactga 860
 Db 908 ggaagagcccaaacacactga 927

RESULT	7
ID	X87265
XX	X87265 standard; cDNA; 927 BP.
XX	
AC	X87265;
XX	
DT	27-SEP-1999 (first entry)
XX	
DE	cDNA clone encoding human PRO509, amplified in tumour cells.
XX	
KW	PRO509; UNQ329; tumour necrosis factor receptor; cancer; diagnosis;
KM	therapy; human; HYEM; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	76..927
FT	/tag= a
PN	MO935170-A2.
PD	
PD	15-JUL-1999.
XX	
PF	05-JAN-1999; 99WO-US00106.
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PR	20-NOV-1998; 98US-0109304.
PR	05-JAN-1998; 98US-0070440.
PR	23-APR-1998; 98US-0083500.
PR	22-MAY-1998; 98US-0086414.
PR	10-JUN-1998; 98US-0088742.
PR	10-NOV-1998; 98US-0107783.
XX	
PA	(GETH) GENENTECH INC.
PI	Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA,
PI	Roy MA, Wood WI;
XX	
DR	WPI; 1999-430385/36.
DR	P-PDB; Y06488.
XX	
PT	Antibody against proteins expressed in neoplastic cells, useful for
PT	tumor diagnosis and treatment
XX	
PS	Example 1; Fig 23; 162pp; English.
XX	
CC	This is the nucleotide sequence of cDNA clone DNA50148 (HYEM)
CC	coding for human PRO509 (UNQ329) (see Y06488), a member of the
CC	tumour necrosis factor receptor family. Amplification of
CC	DNA50148 occurs in various tumours, suggesting an association with
CC	tumour formation or growth. Antagonists (e.g. antibodies) directed
CC	to PRO509 may have use in cancer therapy. The invention identifies
CC	14 genes (see X87254-67) that are amplified in the genome of tumour
CC	cells. Such amplification is expected to be associated with
CC	overexpression of the gene product and to contribute to tumorigenesis
CC	The encoded proteins (see Y06477-90) may be useful targets for the
CC	diagnosis and/or treatment (including prevention) of certain
CC	cancers, and may act as predictors of the prognosis of tumour
CC	treatment.
XX	
Sequence	927BP; 185 A; 286 C; 291 G; 165 T; 0 other;

Query Match	97.4%	Score 858.4	DB 20	Length 927
Best Local Similarity	99.9%	Pred. No. 7,66	209	
Matches	859	Conservative	0	Mismatches 1; Indels 0; Gaps 0

OY	1	ccctagaagatgagacctctctctgagagatgaggggctctctccctctgtgagatccaccccccgaa	60
Db	68	ccctagaagatgagacctctctctgagagatgaggggctctctccctctgtgagatccaccccccgaa	127
OY	61	ccgaagctcttgagcctggtgctgatactcaccttctctggaagccccctgctcaagcccgaa	120

Db	128	cggagcgtctttagagcgtggtgtgtatctcatcttcctcggagagcccccgttaagccccag	167
Qy	121	ctctgacgctctgcaagagagagcagtaaccagctggtgctccgagctgctgcccgaagtga	180
Db	188	ctctgacgctctctgcaagagagagcagtaaccagctggtgctccgagctgctgcccgaagtga	247
Qy	181	gtccagagttatcgtgtgaaagagagcctcgcgvgagagctgcacagvgctgtgtgaaccc	240
Db	248	gtccagagttatcgtgtgaaagagagcctcgcgvgagagctgcacagvgctgtgtgaaccc	307
Qy	241	gcccctccagagacattacatgtgccccactccaatgtgctcaagaagaagtgtctgtacgtccaaa	300
Db	308	gcccctccagagacattacatgtgccccactccaatgtgctcaagaagaagtgtctgtacgtccaaa	367
Qy	301	tgtgtgaacccagacatgctggccgtcgagccgagacatctctccagagagacagaaacgcgcg	360
Db	368	tgtgtgaacccagacatgctggccgtcgagccgagacatctctccagagagacagaaacgcgcg	427
Qy	361	tgtgtgtgtgtgacagcccaagcaccattctgtacatgcttccagagagagagacacatgctgcgcgt	420
Db	428	tgtgtgtgtgtgacagcccaagcaccattctgtacatgcttccagagagagagacacatgctgcgcgt	487
Qy	421	ggccgcgcttaagccacacctccagagcccgagagaggtgcagaaagtgagagacccggagagctc	480
Db	488	ggccgcgcttaagccacacctccagagcccgagagaggtgcagaaagtgagagacccggagagagctc	547
Qy	481	agagacacccctgtgtcagaagaatcgcccccgagagacattctctcccaatgagagccctgtagag	540
Db	548	agagacacccctgtgtcagaagaatcgcccccgagagacattctctcccaatgagagccctgtagag	607
Qy	541	aaatgtcacagaccagaaccaagtgcagctgtgcgtgtgtgacgaaagcccgagagctgtgagcca	600
Db	608	aaatgtcacagaccagaaccaagtgcagctgtgcgtgtgtgacgaaagcccgagagctgtgagcca	667
Qy	601	gctcccaactggtgtgtgtgttctcttccagagagacccctgcatactgtattgtttgtccca	660
Db	668	gctcccaactggtgtgtgtgttctcttccagagagacccctgcatactgtattgtttgtccca	727
Qy	661	cagctgtgacctaatcatatgtgtgaaagaaagaaagcccaaggggtgtatgtatcacaagtga	720
Db	728	cagctgtgacctaatcatatgtgtgaaagaaagaaagcccaaggggtgtatgtatcacaagtga	787
Qy	721	tcgtctccgttccagctgagaaagaaagacagagagctgtgagccacatgtatgtagagccc	780
Db	788	tcgtctccgttccagctgagaaagaaagacagagagctgtgagccacatgtatgtagagccc	847
Qy	781	tgcagagccctctcggaacgttcaacacaggtggtcgtgtgagagacaataccctcatcaacgg	840
Db	848	tgcagagccctctcggaacgttcaacacaggtggtcgtgtgagagacaataccctcatcaacgg	907
Qy	841	ggagagagcccaaacacttga 860	
Db	908	ggagagagcccaaacacttga 927	

RESULT	8
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ID	294198 standard; CDNA; 1634 BP.
XX	
AC	294198;
XX	
DT	19-JUN-2000 (first entry)
XX	
DE	Membrane-bound herpesvirus entry mediator-2 (mHVM2) CDNA
XX	
KW	mHVM-2; membrane-bound herpesvirus entry mediator-2;
KW	TANGO-69; receptor; tumour necrosis factor receptor; human
KW	herpes simplex virus; infection; cancer; inflammation;
KW	autoimmune disorder; therapy; diagnosis; ss.
XX	
OS	Homo sapiens.
XX	

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FH Key          Location/Qualifiers
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FT              /note= "this coding region is separately claimed
FT              in Claim 2"
FT sig_peptide  103..206
FT              /tag= b
FT mat_peptide  207..933
FT              /tag= c
XX
XX WO200014230-A1.
XX
XX 16-MAR-2000.
XX
XX 03-SEP-1999; 99MO-US20180.
XX
XX 03-SEP-1998; 98US-0146950.
XX
XX 29-JUN-1999; 99US-0342767.
XX
XX (MILL-) MILENNIUM BIOTHERAPEUTICS INC.
XX
XX Busfield SJ;
XX
XX WPI; 2000-256981/22.
XX
XX P-PSDB; Y79207.
XX
XX New nucleic acid molecule encoding herpes virus entry mediator (HVEM),
XX either in the soluble or membrane bound form, is useful in screening
XX assays and detection assays.
XX
XX Claim 2; Fig 7; 149pp; English.
XX
XX This full-length DNA sequence, the coding region of which is also
XX claimed, corresponds to CDNA encoding human membrane-bound
XX herpesvirus entry mediator-2 (mhVEM2, see Y79207), a novel form of
XX membrane-bound herpesvirus entry mediator (mhVEM). mhVEM2 is a
XX TANGO-69-receptor and member of the tumour necrosis factor receptor
XX (TNFR) superfamily. The mhVEM2 cDNA, deposited as ATCC 207171,
XX was identified in a human mixed lymphocyte reaction library. HVEM
XX mediates the entry of herpes simplex virus (HSV) into cells. The
XX invention is based on the discovery of 3 cDNA molecules (see
XX 294195-97) which encode soluble forms (see Y79204-06) of mhVEM, and
XX on the present CDNA encoding mhVEM2. In addition to isolated
XX full-length proteins and polynucleotides, and invention provides
XX TANGO-69-receptor fusion proteins, antigenic peptides and
XX antibodies. Also provided are recombinant expression vectors,
XX host cells and transgenic animals in which a TANGO-69-receptor
XX gene has been introduced or disrupted. DNA encoding HVEM, HVEM
XX proteins and HVEM antibodies can be used in screening and detection
XX assays (e.g. chromosomal mapping, tissue typing). HVEM proteins
XX can also be used for regulation of cell proliferation, cell
XX differentiation, cell survival, inflammation mast cell activity,
XX HSV infection and/or proliferation, and/or coagulation. HVEM
XX agonists can be used to treat disorders associated with decreased
XX HVEM activity, e.g. proliferative disorders such as carcinoma or
XX pathogenic infection. Antagonists can be used to treat disorders
XX associated with increased HVEM activity, e.g. autoimmune, T cell,
XX inflammatory and allergic inflammation disorders.
XX
XX Sequence 1834 BP; 398 A; 556 C; 539 G; 341 T; 0 other;
XX
XX
XX Query Match      83.1%; Score 732.4; DB 21; Length 1834;
XX Best Local Similarity 99.9%; Pred. No. 8.4e-177;
XX Matches 733; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 ccgagagcagagagccctcgagagactgggggctccctccctgagagatccaccaccagaa 60
XX |||
XX 95 ccgagagcagagagctccctcgagagactgggggctccctccctgagagatccaccaccagaa 154
XX |||
XX 61 ccgagctcttgagagctggtgctglatctcaccctctcctgagagcccccgtctacgcccag 120
XX |||
XX 155 ccgagctcttgagagctggtgctglatctcaccctctcctgagagcccccgtctacgcccag 214
XX |||

```

```

QY 121 ctctgcgctctcgaagagacagataccag tgggctccgagtgctgcgcccaagtga 180
DB 215 ctctgcgctctcgaagagagacagataccag tgggctccgagtgctgcgcccaagtga 274
QY 181 gtccaggtatcgtgtgaagagagcctgcgggagctgtacagggacacagtgtgtgaacct 240
DB 275 gtccaggtatcgtgtgaagagagcctgcgggagctgtacagggacacagtgtgtgaacct 334
QY 241 ggcctcagagcactcatattggccacctcaatgtgctaagcaagtgtgtcgaatgccaag 300
DB 335 ggcctcagagcactcatattggccacctcaatgtgctaagcaagtgtgtcgaatgccaag 394
QY 301 tgtgtgaccagcagatgggctctgcgagccgagacgtgtcctcagagacagaaagccg 360
DB 395 tgtgtgaccagcagatgggctctgcgagccgagacgtgtcctcagagacagaaagccg 454
QY 361 tgtgtgtgtgacagccagacgtgtcgtcgtcagagagagagagacgtgtgtgtgtgtgt 420
DB 455 tgtgtgtgtgacagccagacgtgtcgtcgtcagagagagagagacgtgtgtgtgtgtgt 514
QY 421 gccgcgcttacgcccactctcagccgagccgagaggtgtcagagagagagacagagatc 480
DB 515 gccgcgcttacgcccactctcagccgagccgagaggtgtcagagagagagacagagatc 574
QY 481 aggaacacctgtgtcagaactgcccccgagacgttctctcccaatggagacctgtgag 540
DB 575 aggaacacctgtgtcagaactgcccccgagacgttctctcccaatggagacctgtgag 634
QY 541 aatgtcagcacacagacaaagtgtgagctgtgtgtcagagagagcgtgtgtgtgtgtgt 600
DB 635 aatgtcagcacacagacaaagtgtgagctgtgtgtcagagagagcgtgtgtgtgtgtgt 694
QY 601 gttcccaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 660
DB 695 gttcccaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 754
QY 661 cagttggcccaatcatatgtgtgaagaagaagcagaggggtgtgtgtgtgtgtgtgtgt 720
DB 755 cagttggcccaatcatatgtgtgaagaagaagcagaggggtgtgtgtgtgtgtgtgtgt 814
QY 721 tcgtctccgtccag 734
DB 815 tcgtctccgtccag 828
XX
XX RESULT 9
XX ID 294195
XX 294195 standard; cDNA; 1929 BP.
XX
XX AC 294195;
XX
XX 19-JUN-2000 (first entry)
XX
XX DE Soluble herpesvirus entry mediator-1 (SHVEM1) cDNA.
XX
XX SHVEM-1: soluble herpesvirus entry mediator-1; TANGO-69-receptor;
XX tumour necrosis factor receptor; human; herpes simplex virus;
XX infection; cancer; inflammation; autoimmune disorder; therapy;
XX diagnosis; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key          Location/Qualifiers
XX FT CDS          297..878
XX FT              /tag= a
XX FT              /note= "this coding region is separately claimed
XX FT              in Claim 2"
XX FT sig_peptide  297..404
XX FT              /tag= b
XX FT mat_peptide  405..875
XX FT              /tag= c
XX

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PN	WO200014230-A1.
XX	
PD	16-MAR-2000.
XX	
PE	03-SEP-1999; 99WO-US02180.
XX	
PR	03-SEP-1998; 98US-0146350.
PR	29-JUN-1999; 99US-0342767.
XX	
PA	(MILL-) MILLENNIUM BIOTHEAPUTICS INC.
XX	
PI	Busfield SJ;
XX	
DR	WPI; 2000-256981/22.
DR	P-PSDB; Y79204.
XX	
PT	New nucleic acid molecule encoding herpes virus entry mediator (HVEM)
PT	either in the soluble or membrane bound form, is useful in screening
PT	assays and detection assays -
XX	
DS	Claim 2; Fig 1; 149pp; English.

This full-length DNA sequence the coding region of which is also claimed, corresponds to cDNA encoding human soluble herpesvirus entry mediator-1 (SHVEM1, see 179204), a novel soluble form of membrane-bound herpesvirus entry mediator (mHVE1). SHVEM1 is a TANGO-69-receptor and member of the tumour necrosis factor receptor (TNFR) superfamily. The SHVEM1 cDNA, deposited as ATCC 98821, was identified in a human aortic endothelial cell cDNA library. SHVEM1 is thought to play a role analogous to other soluble members of the TNFR superfamily by interfering with the ability of LIGHT-TANGO-69 and lymphotoxin to bind mHVE1, and to play a role in herpes simplex virus (HSV) entry. The invention is based on the discovery of 3 cDNA molecules (see 294195-97) which encode soluble forms (see 179204-06), and 1 cDNA molecule (see 294198) that encodes a 2nd membrane-bound form (see 179207), of mHVE1. In addition to isolated full-length proteins and polynucleotides, and invention provides TANGO-69-receptor fusion proteins, antigenic peptides and antibodies. Also provided are recombinant expression vectors, host cells and transgenic animals in which a TANGO-69-receptor gene has been introduced or disrupted. DNA encoding HVE1, HVE1 proteins and HVE1 antibodies can be used in screening and detection assays (e.g. chromosomal mapping, tissue typing). HVE1 proteins can also be used for regulation of cell proliferation, cell differentiation, cell survival, inflammation mast cell activity, HSV infection and/or proliferation, and/or coagulation. HVE1 agonists can be used to treat disorders associated with decreased HVE1 activity, e.g. proliferative disorders such as carcinoma or pathogenic infection. Antagonists can be used to treat disorders associated with increased HVE1 activity, e.g. autoimmune, T cell, inflammatory and allergic inflammation disorders.

SD Sequence 1929 BP; 384 A; 614 C; 565 G; 366 T; 0 other;

Query Match	78.2%;	Score 688.8;	DB 21;	Length 1929;
Best Local Similarity	82.9%;	Pred. No. 9.8e-166;		
Matches 879; Conservative	0;	Mismatches 2;	Indels .179;	Gaps 1.

QY	1	cctaaagcattggaacccctccctggagagactgggggctcctctccctgtgaatccacccccaagaa	60
Db	289	ccctgaaggacatggaacccctccctggaaacactgggggctcctccctctgtgaatccacccccaagaa	348
QY	61	ccgaagctcttgaagctctgtgtctgtatctacactcctcctgtagagccccctgtctaacgcccacag	120
Db	349	ccgaagctcttgaagctctgtgtctgtatctacactcctcctgtagagccccctgtctaacgcccacag	408
QY	121	ctctgcgcgtctctgtaagaaggaagacagatcaaccacagttgggctcccgagtgctgcccccaagtgcga	180
Db	409	ctctgcgcgtctctgtaagaaggaagacagatcaaccacagttgggctcccgagtgctgcccccaagtgcga	468
QY	181	gtccagagttatcgtgtatgaagaagagcctcctgctggggagctgcagcgggcacacagtgctgtgaacct	240

[illegible]

XX Homo sapiens.
 OS
 XX
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 CDS 107..700
 FT /*tag= a
 FT /note= "this coding region is separately claimed
 FT sig-peptide 107..220
 FT /*tag= b
 FT mat-peptide 221..697
 FT /*tag= c
 XX
 PN WO200014230-A1.
 XX
 PD 16-MAR-2000.
 XX
 PF 03-SEP-1999; 99WO-US20180.
 XX
 PR 03-SEP-1998; 98US-0146950.
 PR 29-JUN-1999; 99US-0342767.
 XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 PI Busfield SJ;
 DR WPI: 2000-256981/22.
 DR P-PSDB; Y79205.
 XX
 PT New nucleic acid molecule encoding herpes virus entry mediator (HVE),
 PT either in the soluble or membrane bound form, is useful in screening
 PT assays and detection assays -
 PS
 PS Claim 2; Fig 3; 149pp; English.
 XX
 CC This full-length DNA sequence, the coding region of which is also
 CC claimed, corresponds to cDNA encoding human soluble herpesvirus
 CC entry mediator-2 (SHVEM2, see Y79205), a novel soluble form of
 CC membrane-bound herpesvirus entry mediator (mHVE). SHVEM2 is a
 CC TANGO-69-receptor and member of the tumour necrosis factor receptor
 CC (TNFR) superfamily. The SHVEM2 cDNA, deposited as ATCC 207173, was
 CC identified in a human aortic endothelial cell cDNA library. SHVEM2
 CC is thought to play a role analogous to other soluble members of the
 CC TNFR superfamily by interfering with the ability of LIGHT-TANGO-69
 CC and lymphotoxin to bind mHVE, and to play a role in herpes simplex
 CC virus (HSV) entry. The invention is based on the discovery of 3
 CC cDNA molecules (see Z94195-97) which encode soluble forms (see
 CC Y79204-06), and 1 cDNA molecule (see Z94198) that encodes a 2nd
 CC membrane-bound form (see Y79207), of mHVE. In addition to
 CC isolated full-length proteins and polynucleotides, and invention
 CC provides TANGO-69-receptor fusion proteins, antigenic peptides and
 CC antibodies. Also provided are recombinant expression vectors,
 CC host cells and transgenic animals in which a TANGO-69-receptor
 CC gene has been introduced or disrupted. DNA encoding HVE, HVE
 CC proteins and HVE antibodies can be used in screening and detection
 CC assays (e.g. chromosomal mapping, tissue typing). HVE proteins
 CC can also be used for regulation of cell proliferation, cell
 CC differentiation, cell survival, inflammation mast cell activity,
 CC HSV infection and/or proliferation, and/or coagulation. HVE
 CC agonists can be used to treat disorders associated with decreased
 CC HVE activity, e.g. proliferative disorders such as carcinoma or
 CC pathogenic infection. Antagonists can be used to treat disorders
 CC associated with increased HVE activity, e.g. autoimmune, T cell,
 CC inflammatory and allergic inflammation disorders.
 XX
 SQ Sequence 1596 BP; 341 A; 485 C; 483 G; 287 T; 0 other;

Query Match 76.28; Score 671.4; DB 21; Length 1596;
 Best Local Similarity 84.94; Pred. No. 2.4e-161;
 Matches 780; Conservative 0; Mismatches 101; Indels 38; Gaps 1;
 QY 1 cctgagcatgagcctctctgagactgaggcctctccctgagatccacccccagaa 60

DB 99 cctgagcatgagcctctctgagactgaggcctctccctgagatccacccccagaa 158
 QY 61 ccgaagcttgagagctgtgtctgtatctcaaccttcctggagagccccctgtacagccag 120
 DB 159 ccgagctcttgagagctgtgtctgtatctcaaccttcctggagagccccctgtacagccag 218
 QY 121 cctgagcctctgcaagagagacagatccacagtgagctccagatgtgtcccaagtga 180
 DB 219 cctgagcctctgcaagagagacagatccacagtgagctccagatgtgtcccaagtga 278
 QY 181 gtcgaagtatcgttgaaagagagcctgagggagagctgtacagggacagtggtgaacct 240
 DB 279 gtcgaagtatcgttgaaagagagcctgagggagagcctgagggacagtggtgaacct 338
 QY 241 gccctcagagcactatattgcccactcaatgagcctcaagcaagtgtctcagtgccaa 300
 DB 339 gccctcagagcactatattgcccactcaatgagcctcaagcaagtgtctcagtgccaa 388
 QY 301 tgtgtgacccagccatgagctgtgagcagagccagagctgtcagagacagagacgcg 360
 DB 399 tgtgtgacccagccatgagctgtgagcagagccagagctgtcagagacagagacgcg 458
 QY 361 tgtgtgagcagccagccactctgcaatcgtgcagagacagagagcagagcagcgcgt 420
 DB 459 tgtgtgagcagccagccactctgcaatcgtgcagagacagagagcagagcagcgcgt 518
 QY 421 gccgagcttcagccacttcacagccagagagagagagagagagagagagagagagc 480
 DB 519 gccgagcttcagccacttcacagccagagagagagagagagagagagagagagagc 578
 QY 481 agagacccctgtgtcaaatctgcccccgaggagacctctcccaatgagagccttgagg 540
 DB 579 agagacccctgtgtcaaatctgcccccgaggagacctctcccaatgagagccttgagg 638
 QY 541 aatgtacagcaccagaccaaagt----- 562
 DB 639 aatgtacagcaccagaccaaattgtcctaatcatatgtgtgaagaagaagccaagaggt 698
 QY 563 cagctgtgtgtgaagagagccagagctgtgagcagagctccacagtggtatgtgtgt 622
 DB 699 gagacacagcagccagccatcagagctcatgtatgtccacagcgtcttgagctgtgt 758
 QY 623 tcttcagagagcctgtctcatgtcatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 682
 DB 759 accccaagccttgagagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 818
 QY 683 gaaagaagaagcagagagtgatgtatgaagtgatcgtgtgtgtgtgtgtgtgtgtgt 742
 DB 819 gccactgagcgt 878
 QY 743 acaggaagcaggaagtgagcagacagatcattgagccttcagagccttcagagctcac 802
 DB 879 acaggaagcaggaagtgagcagacagatcattgagccttcagagccttcagagctcac 938
 QY 803 cagcgtgagcgtgtgagagacatattcctcatcagggagagagacccaacactgacc 862
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 QY 863 cacagactgaccccca 881
 DB 999 cacagactgaccccca 1017
 RESULT 11
 Z94197
 ID Z94197 standard; cDNA; 2313 BP.
 XX
 AC Z94197;
 XX
 DT 19-JUN-2000 (first entry)
 XX Soluble herpesvirus entry mediator-3 (SHVEM3) cDNA.

XX SHVEM-3; soluble herpesvirus entry mediator-3; TANGO-69-receptor;
 KW tumour necrosis factor receptor; human; herpes simplex virus;
 KW infection; cancer; inflammation; autoimmune disorder; therapy;
 KW diagnosis; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 85..645
 FT /tag= a
 FT /note= "this coding region is separately claimed
 In Claim 2"

FT sig_peptide 85..198
 FT /tag= b
 FT mat_peptide 199..642
 FT /tag= c

XX WO200014230-A1.

XX 16-MAR-2000.

XX 03-SEP-1999; 99MO-US20180.

XX 03-SEP-1998; 98US-0146950.

XX 29-JUN-1999; 99US-0342767.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX Busfield SJ;

XX WPI: 2000-256981/22.

XX P-PSDB; Y79206.

XX New nucleic acid molecule encoding herpes virus entry mediator (HVEM),
 PT either in the soluble or membrane bound form, is useful in screening
 PT assays and detection assays -

XX Claim 2; Fig 5; 149pp: English.

XX This full-length DNA sequence, the coding region of which is also
 CC claimed, corresponds to cDNA encoding human soluble herpesvirus
 CC entry mediator-3 (SHVEM3, see Y79206), a novel soluble form of
 CC membrane-bound herpesvirus entry mediator (mHVEM). SHVEM3 is a
 CC TANGO-69-receptor and member of the tumour necrosis factor receptor
 CC (TNFR) superfamily. The SHVEM3 cDNA, deposited as AFCC 207172, was
 CC identified in a human mixed lymphocyte reaction library. SHVEM3
 CC is thought to play a role analogous to other soluble members of the
 CC TNFR superfamily by interfering with the ability of LIGHT-TANGO-69
 CC and lymphotoxin to bind mHVEM, and to play a role in herpes simplex
 CC virus (HSV) entry. The invention is based on the discovery of 3
 CC cDNA molecules (see 294195-97) which encode soluble forms (see
 CC Y79204-06), and 1 cDNA molecule (see 294198) that encodes a 2nd
 CC membrane-bound form (see Y79207), of mHVEM. In addition to
 CC isolated full-length proteins and polynucleotides, and invention
 CC provides TANGO-69-receptor fusion proteins, antigenic peptides and
 CC antibodies. Also provided are recombinant expression vectors,
 CC host cells and transgenic animals in which a TANGO-69-receptor
 CC gene has been introduced or disrupted. DNA encoding HVEM, HVEM
 CC proteins and HVEM antibodies can be used in screening and detection
 CC assays (e.g. chromosomal mapping, tissue typing). HVEM proteins
 CC can also be used for regulation of cell proliferation, cell
 CC differentiation, cell survival, inflammation mast cell activity,
 CC HSV infection and/or proliferation, and/or coagulation. HVEM
 CC agonists can be used to treat disorders associated with decreased
 CC HVEM activity, e.g. proliferative disorders such as carcinoma or
 CC pathogenic infection. Antagonists can be used to treat disorders
 CC associated with increased HVEM activity, e.g. autoimmune, T cell,
 CC inflammatory and allergic inflammation disorders.

XX Sequence 2313 BP; 411 A; 762 C; 689 G; 451 T; 0 other;

Query Match 63.18; Score 555.8; DB 21; Length 2313;
 Best Local Similarity 99.6%; Pred. No. 5.6e-132;
 Matches 557; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cctgagcatggaagccctcctggaagactgggggctctcctctgtagatccaaccccgaa 60
 DB 77 cctgagcatggaagccctcctggaagactgggggctctcctctgtagatccaaccccgaa 136
 QY 61 ccgacgcttgagcgtgtgtatctcaactcctccggagacccctgtacgcccag 120
 DB 137 ccgacgcttgagcgtgtgtatctcaactcctccggagacccctgtacgcccag 196
 QY 121 cctcgcctcctgcaagagagacagatcccaatgggctcgaagtgtcgtcccaagtca 180
 DB 197 cctcgcctcctgcaagagagacagatcccaatgggctcgaagtgtcgtcccaagtca 256
 QY 181 gtcaggtatcgtgtgaagagagcctcgtgggagcgtcgaagcgagacgtgtgaaacct 240
 DB 257 gtcaggtatcgtgtgaagagagcctcgtgggagcgtcgaagcgagacgtgtgaaacct 316
 QY 241 gccctcagagcaactatgcccacactcaatggccttaagcaagtgtcgaagtccaaa 300
 DB 317 gccctcagagcaactatgcccacactcaatggccttaagcaagtgtcgaagtccaaa 376
 QY 301 tgtgtgacccagcatgtggcctcgcgagccggaactgtctccagagacagaaacgcg 360
 DB 377 tgtgtgacccagcatgtggcctcgcgagccggaactgtctccagagacagaaacgcg 436
 QY 361 tgtgtgttcagccagccagcactctgcactgtcagagcagcgagacacatggtccgct 420
 DB 437 tgtgtgttcagccagccagcactctgcactgtcagagcagcgagacacatggtccgct 486
 QY 421 gccgccttaagccacactccagcccgccagagaggtgcagaagggagccagagatc 480
 DB 497 gccgccttaagccacactccagcccgccagagaggtgcagaagggagccagagatc 556
 QY 481 aggaacacctgtgtcagaactgcccccgaggacctctctccaatggaacctgagag 540
 DB 557 aggaacacctgtgtcagaactgcccccgaggacctctctccaatggaacctgagag 616
 QY 541 aatgtacagaccagaccaa 559
 DB 617 aatgtacagaccagaccaa 635

RESULT 12

ID V34510 standard: cDNA; 2692 BP.

XX V34510;

DT 25-SEP-1998 (first entry)

XX Human TNF receptor related splice variant 1 (TR2-SV1) gene.

XX de: human; tumour necrosis factor; TNF; herpes simplex virus;

KW aberrant cell survival; radiation therapy; lymphocyte proliferation;
 KW immune deficiency syndrome.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 373..930

XX sig_peptide /tag= a /product= "TR2 protein"

XX mat_peptide /tag= b /tag= c

XX WO9818824-A1.

XX 07-MAY-1998.

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2001, 16:55:20 ; Search time 1458.62 Seconds
(without alignments)
8279.381 Million cell updates/sec

Title: US-08-741-095b-25
Perfect score: 881
Sequence: 1 cctgagcagtgcagctcct.....ccacagactctgcaccccca 881

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 118133 seqs, 6853842396 residues
Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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67: gb_htg20:*
68: gb_htg21:*
69: gb_htg22:*
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73: gb_ba3:*
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81: gb_pat1:*
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83: em_htg90:*
84: gb_htg24:*
85: gb_pr8:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	879.4	99.8	1681	37	AF153978	AF153978 Homo sapi
2	879.4	99.8	1704	13	AX022023	AX022023 Sequence
3	879.4	99.8	1704	78	HSU81232	U81232 Human tumor
4	879.4	99.8	1724	78	HSU70321	U70321 Human tumor
5	869	78.2	852	37	AF147720	AF147720 Chloroce
6	342.2	38.8	2692	13	AX022026	AX022026 Sequence
7	239.4	27.2	2637	13	AX022029	AX022029 Sequence
8	160.6	18.2	154530	66	AL139246	AL139246 Homo sapi
9	89	10.1	154530	66	AL139246	AL139246 Homo sapi
10	76.4	8.7	837	3	AX027018	AX027018 Sequence
11	76.4	8.7	845	3	AX027450	AX027450 Sequence
12	60.8	6.9	2136	85	HUMTNRFP	L04270 Homo sapien
13	60.8	6.9	2148	37	AK027080	AK027080 Homo sapi
14	60.4	6.9	2394	85	HUMTNRFP	M55994 Human tumor
15	59.6	6.8	691	81	I36350	I36350 Sequence 12
16	58	6.6	1557	81	I36197	I36197 Sequence 3
17	58	6.6	1641	81	I36196	I36196 Sequence 1
18	58	6.6	2253	81	A78517	A78517 Sequence 1
19	58	6.6	3380	79	G26865	G26865 human STS S
20	58	6.6	3492	85	S63368	S63368 tumor necro
21	58	6.6	3683	85	HUMNFR	M32315 Human tumor

22	57	6.5	834	48	AX027007	Sequence
23	57	6.5	1004	78	X60592	Human CD40
24	57	6.5	1004	81	I07284	Sequence 31
25	55.8	6.3	519	81	AR076920	Sequence
26	55.8	6.3	519	81	AR078310	Sequence
27	55.8	6.3	519	81	AR085413	Sequence
28	55.4	6.3	807	3	AX027021	Sequence
29	55.4	6.3	815	3	BTU57745	Bos taurus
30	53.8	6.1	1614	11	MUSLYMPHOB	Mus musculus
31	53.8	6.1	2076	11	MMU29173	Mus musculus
32	52.6	6.0	870	11	AX027014	Sequence
33	52.6	6.0	1579	11	MUSCD40A	Sequence
34	49.4	5.6	5820	71	AF145588	Stealth v
35	48.6	5.5	1017	11	RSOX40	Sequence
36	47.8	5.4	4181	8	AB029021	Human sapi
37	47.8	5.4	174253	57	AC068590	Human sapi
38	47.4	5.4	157634	55	AC060233	Human sapi
39	47.4	5.4	180188	40	AC015656	Human sapi
40	47.4	5.4	187966	9	AC006487	Human sapi
41	47.2	5.4	1600	81	AA3530	Sequence 1
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44	46.2	5.2	1505	11	MUSMTFR2	Mus tumor
45	46.2	5.2	3796	11	M59378	Murine tumor

ALIGNMENTS

RESULT 1
LOCUS AF153978 1681 bp mRNA PRI 13-JUN-2000
DEFINITION Homo sapiens CD40-like protein precursor mRNA, complete cds.
ACCESSION AF153978
VERSION AF153978.1 GI:8489096

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1681) Zhang, W., Wan, T. and Cao, X.
AUTHORS Direct Submission
TITLE Submitted (25-MAY-1999) Department of Immunology, Second Military Medical University & Shanghai Brilliance Biotechnology Institute, 800 Xiangyin Road, Shanghai 200433, P.R. China
JOURNAL Location/Qualifiers

FEATURES

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LCQNPPTGTFSPNGTLEBCOHTKCSMLVTKAGAGTSSHWMLSGSLVIVICST
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TGRSPNH"

BASE COUNT 336 a 520 c 499 g 326 t
ORIGIN

Query Match 99.8%; Score 879.4; DB 37; Length 1681;
Best Local Similarity 99.9%; Pred. No. 6.7e-181;
Matches 880; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ccctgaagcattgagcctctcctgagactggggcctctcctctggaatacaccaccagaa 60
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DB 238 CCTGAGGCAATGAGCCTCTGAGACTGGGGGCTCTCTCCCTGAGAGATCACCCCAAAA 297

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DB	298	CCGACGCTCTTGAGAGCTGTGCTGTATCTCACCTTCTCTGGAGAGCCCTCTAGGCCCCAG	357
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DB	358	CTCTGCCGCTCTCCAGAGGAGAGAGAGTACCACTGGGCTCCGAGTCTCCCAATGTGA	417
QY	181	gtcccaagtatctgtgtgaagagagcctctgagagagcttgcacgagatgttgaacct	240
DB	418	GTCACAGTATCTGTGAAGAGGCTGCGGGAGCTGACGGGACAGTGTGTGAACCT	477
QY	241	gacctccagacactcatctgcccacactcaatgagccttaagcaagtgctcgcagtgcaaa	300
DB	478	GCCCTCCAGGACCTTATGCTGAGAGGCTGCGGGAGCTGACGGGACAGTGTGTGAACCT	537
QY	301	tgtgtgacccagcattgagcctctgcgcgagagccggaactgtctccagagacagaaacgcg	360
DB	538	TGTGTGACCCAGCATTGAGGCTGCGGGAGCTGCGGGAGCTGACGGGACAGTGTGTGAACCT	597
QY	361	tgtgtgtgtgagcagcagcagcactctgtcatctgctccagagagagacacttgccgcggt	420
DB	598	TGTGTGTGTGACCCAGCCTTCTGATCTGTCAGAGAGGAGGACACTGCGCGCT	657
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QY	541	aatgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	600
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DB	838	GTCGCCAGTGGGATGT	897
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RESULT 2
LOCUS AX022023 1704 bp DNA UNA 07-SEP-2000
DEFINITION Sequence 1 from Patent EP0961782.
ACCESSION AX022023
VERSION AX022023.1 GI:10045729
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1704)
AUTHORS Hurler, M.R., Lyn, S.D., Ni, J., Rosen, C.A. and Gentz, R.L.
TITLE Human tumor necrosis factor receptor-like 2
JOURNAL Patent: EP 0961782-A 08-DEC-1999;
HUMAN GENOME SCIENCES INC (US); SMITHKLINE BEECHAM CORP (US)
FEATURES Location/Qualifiers

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/translation="MEPPDGMGPPWRSPKTDVRLVLYLFLGAPCYAPALPSCKE
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TGRSPNH"
mat_peptide 373..1113
BASE COUNT 343 a 529 c 504 g 328 t
ORIGIN

Query Match 99.8%; Score 879.4; DB 13; Length 1704;
Best Local Similarity 99.9%; Pred. No. 6.7e-181;
Matches 880; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 61 ccgagctcttgagcgtggtgtgtatctcaacctcttgagagccctctgtaagcccccag 120
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QY 121 cctctgcgtctctcaaggaagagacagataccagttggcctcagagttcgtcccaagtga 180
DB 377 CTCTGCCGTCTCTCAAGAGAGAGAGAGTACCAATGGGCTCCGAGTGTGCGCCCAATGCA 436
QY 181 gtcccaagttacgtgtgaaggaagcctcggagagctgacagggcagacagttgtgaacct 240
DB 437 GTCCAGAGTTATCGTGTGAAGAGAGGCTGCGGGAGCTGACGGGACACAGTGTGAACCTT 496
QY 241 ggcctcagagcactatcatctgcccactcaatgtgcttaagcaagtgtctgcaatgcca 300
DB 497 GCCCTCCAGGACCTACATTTGCCACCTCAATGGCTTAACAGATCTCTGCACTGCCAAA 556
QY 301 tctgtacaccagcattgagcctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 360
DB 557 TGTGTACCCAGGACATGGGCTGCGGCGGCGGAGAACTCTCCAGAGACAGAACGCCG 616
QY 361 tctgtgtgttgagcagccagcactctctgacgtctcagagaaggggaaccatgcgcgct 420
DB 617 TGTGTGTTGCAAGCCAGGCGCACTTCTGCTCAGAGAGGAGGAGCACTGCGCGCGCT 676
QY 421 ggcgcgttaagcagcactcagcccgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 480
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QY 481 aggaacacctgtgtcagaaactgcccccgggagccttctctcccaatggagacccctgag 540
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QY 541 aatgtacagcagaccaaagtcagctggtgtgaaggaagcgcgcgcgcgcgcgcgcgcgcgc 600
DB 797 AATGTACAGCACCAAGTGTGAGCTGTGCTGACGAAAGGCGGAGGCTGGAGACAGCA 856
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RESULT 3
HSU81232
LOCUS HSU81232 1704 bp mRNA PRI 05-JAN-1999
DEFINITION Human tumor necrosis factor receptor-like gene 2 (TR2) mRNA,
complete cds.
ACCESSION U81232
VERSION U81232.1 GI:4098958
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1704)
AUTHORS Kwon,B.S., Tan,K.B. and Ni,J.
TITLE A newly-identified member of the tumor necrosis factor receptor
superfamily with a wide tissue distribution and involvement in
lymphocyte activation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1704)
AUTHORS Ni,J.
TITLE Direct Submission
JOURNAL Submitted (06-DEC-1996) Protein Expression and Purification, Human
Genome Sciences, Inc., 9410 Key West Ave., Rockville, MD
20850-3338, USA

FEATURES
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TGRSPNH"

BASE COUNT 343 a 529 c 504 g 328 t
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Query Match 99.8%; Score 879.4; DB 78; Length 1704;
Best Local Similarity 99.9%; Pred. No. 6.7e-181;
Matches 880; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 cctgagagcatgagcctcctctgagactggggcctcctcccttgagagatccacccacagaa 60
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QY 61 ccgagctcttgagcgtggtgtgtatctcaacctcttgagagccctctgtaagcccccag 120
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[illegible]

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Matches 880; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
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OY	61 ccgacgctctgagagctggtgctgtatctcacccttcgysagccccctgtaagcccgag 120
Db	346 CCGAGCTTGTGAGCTGGTGTGTATCTACACTTCTCGAGAGCCCTGTACAGCCCGAG 405
OY	121 ctctgcgctctctgcaagaaagacagatgcccaagtggtgtccgaatgctgcccccaagtga 180
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OY	181 gtccaggtctatcgtctgaaagagagcgtcgcgggagctagagcgacagtgtgtaacct 240
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DEFINITION	Chlorocephus aethiops hveas (hveas) mRNA, complete cds.		
ACCESSION	AF147720		
VERSION	AF147720.1	GI:5002247	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
SOURCE			
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CDS			
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Best Local Similarity	90.7%;	Pred. No. 1.5e-139;	Length 852;
Matches	770;	Conservative 0;	Mismatches 70;
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QY	129	tccctcaaggaagaaatataccagttggtctccgagtctgcctcccaagtgaftccaagt	180
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QY	249	ggcaccataatgtgccaccataatgtgacctaaagcaagtgltctgcagtgccaaatgtgtac	300
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QY	549	caccagaccagaatgtagc---tgagctgttgaagagagccgaagcttggagaccagaagctcc	600
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LOCUS	AX022026	2692 bp DNA	UNA
DEFINITION	Sequence 4 from Patent EP0961782.		07-sep-2000
ACCESSION	AX022026		
VERSION	AX022026.1	GI:10045731	
KEYWORDS			
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 2692)		
AUTHORS	Huile,M.R., Lym,S.D., Ni,J., Rosen,C.A. and Gentr,R.L.		
TITLE	Human tumor necrosis factor receptor-like 2		


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VERSION
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

OY      489      ctctgtcagaactctcccccgaggacc 515
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VERSION
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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

RESULT  9
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LOCUS   154530 bp DNA HTG 10-AUG-2000
DEFINITION Homo sapiens chromosome 1 clone RP3-395M20 map p36.11-36.33, ***
SEQUENCING IN PROGRESS ***, 6 unordered pieces.
ALI39246
ALI39246.6 GI:9796372
HTG; HTGS_PHASE1; HTGS_DNAFLT.
human.
Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 154530)
Plumb, B.
Submitted (09-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humbureys@sanger.ac.uk
requests: clonerquest@sanger.ac.uk
On Aug 11, 2000 this sequence version replaced gi:9367391.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humbureys@sanger.ac.uk
----- Project Information
Center project name: dj395M20
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 152602 bases at least Q40
Consensus quality: 153318 bases at least Q30
Consensus quality: 153701 bases at least Q20
Insert size: 154030; sum-of-contigs
Insert size: 167102; 1.8% error; agarose-fp
Quality coverage: 6.88x in Q20 bases; sum-of-contigs Quality
coverage: 6.34x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 23698: contig of 23698 bp in length
* 23699 23798: gap of 100 bp
* 23799 46060: contig of 22262 bp in length
* 46061 46160: gap of 100 bp
* 46161 100189: contig of 54029 bp in length
* 100190 100289: gap of 100 bp
* 100290 108179: contig of 7890 bp in length
* 108180 108279: gap of 100 bp
* 108280 129035: contig of 20756 bp in length
* 129036 129135: gap of 100 bp
* 129136 154530: contig of 25395 bp in length.
*
* Location/Qualifiers
* 1 . 154530

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
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/clone_lib="RPCI-3"
1. 23698
/feature="assembly_fragment:00746"
fragment_chain:1"
misc_feature
23799.46060
/feature="assembly_fragment:00410"
fragment_chain:1"
misc_feature
46161.100189
/feature="assembly_fragment:00468"
fragment_chain:1"
misc_feature
100290.108179
/feature="assembly_fragment:02473"
fragment_chain:2"
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BASE COUNT 29475 a 48692 c 47274 g 28589 t 500 others
ORIGIN

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Query Match 10.18; Score 89; DB 66; Length 154530;
Best Local Similarity 75.98; Pred. No. 4.8e-10;
Matches 110; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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QY 562 gcagctgctgtgtacgaagccgagctgtgaccacagctccactgggtatgtcgt 621
|||||
Db 144081 GCAGGTGCTGTGTACGAGCCGACGACCTGTGGACACAGCTCCGCTGGGTGATTC 144022
|||||
QY 622 ttctctcaaggagctgtcgtatgttctgtccacagttggcctaatacatatgtg 681
|||||
Db 144021 TCTCAGGAGCCTCATCTCATCATCTGATTTCTCACACTGTGGCTATCTCATGCA 143962
|||||
QY 682 tgaagaagaagaagcgaagggtga 706
|||||
Db 143961 TGAAGAAGAAGAATCAAGGGTGA 143937

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RESULT 10
LOCUS AX027018 837 bp DNA MAM 16-SEP-2000
DEFINITION Sequence 15 from Patent WO0037102.
ACCESSION AX027018
VERSION AX027018.1 GI:10188046
KEYWORDS
SOURCE
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 837)
AUTHORS
Rogers,N.J., Dörfling,A. and Lechler,R.I.
TITLE
Immunosuppression
JOURNAL
Patent: WO 0037102-A 29-JUN-2000;
ROGERS NICHOLA JANE (GB) ; DÖRLING ANTHONY (GB) ; ML LAB PLC (GB) ;
LECHLER ROBERT IAN (GB)
FEATURES
source
1. 837
Location/Qualifiers
/organism="Sus scrofa"
/db_xref="taxon:9823"
BASE COUNT 207 a 231 c 221 g 178 t
ORIGIN

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Query Match 8.78; Score 76.4; DB 3; Length 837;
Best Local Similarity 51.08; Pred. No. 1e-06;
Matches 213; Conservative 0; Mismatches 196; Indels 9; Gaps 1;

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QY 103 cccctctctacgccccagctctgcgtctctgtcaagaagagagtaaccagttggtccg 162
|||||
Db 47 CCGCGCTCCACACCAGAACCCACCACTTCATGCAAGAAACCAATATCCACACAACAGCC 106
|||||
QY 163 agtgcgtcccaagtgagtcagtcaggtatctgttgaagagaggtccggtgagctacgg 222
|||||
Db 107 GGTGCTTAATTTGTGCGCCGACAGAGCAAGAACTGGTAACCACTGCACAGAGTCACTG 166
|||||
QY 223 gacagtggttgaaacctgtccctccagacacacacacacacacacacacacacacac 282
|||||
Db 167 AACAGAGATGCTTCTTGTGAGTTCCAGCAATTTCTAGCACTGTGAATAGAGAGAAC 226
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QY 283 agtgcgtcagtgccaaatgtgtgacccacacacacacacacacacacacacacacac 342
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Db 227 ACGTGATATGACCAATAATATGAGACCCCACTAGGTCTCCAGGTCCAGAGGAGGCA 286
|||||
QY 343 ccaggaagaagaagccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 402
|||||
Db 287 CCTCGAAGAACAGACACCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 346
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QY 403 gggagccactgcccgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 462
|||||
Db 347 GTGAAGTTGCACTTGTG-----CACAGCTTGTGCTTCCCTGGCTCGGGTCAAGC 397
|||||
QY 463 agggagcaccagagagtcagagacacccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 520
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Db 398 AGATGGCGACAGAGGTTTCTGACATATCTGTGAACCCCTGCCAGTTGGCTTCTTC 455

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RESULT 11
LOCUS AX027450 845 bp DNA MAM 16-SEP-2000
DEFINITION Sequence 3 from Patent WO0039294.
ACCESSION AX027450
VERSION AX027450.1 GI:10188416
KEYWORDS
SOURCE
ORGANISM
Sus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 845)
AUTHORS
Bravery,C., Thompson,S. and Rushworth,S.
TITLE
Porcine cells incapable of expressing cd40 antigen, for
xenotransplantation
JOURNAL
Patent: WO 0039294-A 06-JUL-2000;
NOVARTIS ERIND VERNALT GMBH (AT) ; NOVARTIS AG (CH) ; BRAVERY
CHRISTOPHER (GB) ; THOMPSON SIMON (GB) ; RUSHWORTH STUART (GB)
FEATURES
source
1. 845
Location/Qualifiers
/organism="Sus sp."
/db_xref="taxon:9826"
BASE COUNT 206 a 237 c 224 g 178 t
ORIGIN

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Query Match 8.78; Score 76.4; DB 3; Length 845;
Best Local Similarity 51.08; Pred. No. 1e-06;
Matches 213; Conservative 0; Mismatches 196; Indels 9; Gaps 1;

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QY 103 cccctctctacgccccagctctgcgtctctgtcaagaagagagtaaccagttggtccg 162
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Db 55 CCGCGCTCCACACCAGAACCCACCACTTCATGCAAGAAACCAATATCCACACAACAGCC 114
|||||
QY 163 agtgcgtcccaagtgagtcagtcaggtatctgttgaagagaggtccggtgagctacgg 222
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Db 115 GGTGCTTAATTTGTGCGCCGACAGAGCAAGAACTGGTAACCACTGCACAGAGTCACTG 174
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QY 223 gacagtggttgaaacctgtccctccagacacacacacacacacacacacacacacac 282
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Db 175 AACAGAGATGCTTCTTGTGAGTTCCAGCAATTTCTAGCACTGTGAATAGAGAGAAC 234
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QY 283 agtgcgtcagtgccaaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 342
|||||

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RESULT	12	
HUMTNFRP		
LOCUS		
DEFINITION	HUMTNFRP 2136 bp mRNA	PR1 03-AUG-1993
ACCESSION	Homo sapiens (clone CD18) tumor necrosis factor receptor 2 related protein mRNA, complete cds.	
VERSION	L04270	
KEYWORDS	L04270.1 GI:339761	
SOURCE	tumor necrosis factor receptor 2 related protein.	
ORGANISM	Homo sapiens (library: Liver cDNA of P.M.) Liver cDNA to mRNA.	
REFERENCE	Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	Baens, M., Chaffanel, M., Cassiman, J.J., Van den Berghe, H. and Maymen, P.	
TITLE	Construction and evaluation of a hncDNA library of human 12p transcribed sequences derived from a somatic cell hybrid	
JOURNAL	Genomics 16, 214-218 (1993)	
MEDLINE	93252381	
FEATURES		
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	169..1476	
	/note="putative"	
	/codon_start=1	
	/product="tumor necrosis factor receptor 2 related protein"	
	/protein_id="AAA36757.1"	
	/db_xref="GI:339762"	
	/translation="MLPMWATSAPGLAMGLVGLFGLLAASQPAVPPVASENQCRCDOEVEYEPQHRICCSRCSPPTVYSACSRIDVVCATCENSYNEHMYLITCOLCRPCPWRNIEIAPCTSRKTCQRCOPMFCRMALECTHELSDCPGEAEALKDEVAKGKNGHCVPCIAKGFHONTSSPSCOPHRENGGLIEAAGVTAOSDPTCKNPLEPLPMSMGTLMLAVILPLAFLLIATVAFSCIMKSHPSLRKGLSLKRRPOGSGPVPVGSWEPRKHPFRFDPDVLPLPISGVSVSYSTGLPAPVLEAGVPOQSGPLDITREPQLEPGEDSOVAHGNGIHVYTGSGMTTGNITLYINGVLPVGPPEGVDLPATPEPPYPIPEGGDPGPPGSTPHOEDGKAMHLAETHENCACTPSNRQPMOFTIHD"	
BASE COUNT	446 a 706 c 608 g 376 t	
ORIGIN		
Query Match	6.9%; Score 60.8; DB 85; Length 2136;	
Best Local Similarity	51.5%; Pred. No. 0.0019;	
Matches 140: Conservative	0; Mismatches 132; Indels 0; Gaps 0;	
OY	135 aaggaagcagcgtaccacagtgctgcgaagtcgtgcccccaagtcgaatgcacaggtatcgt	194
Db	310 AAGGAATCTATGAGACCCACACCGCATCTGCTCCCTGCCGCCAGGCACCTAT	369
OY	195 gtgaagagcgtcgtggggaagctga-cgggacagtgctgaaacctgcctccaaagcaac	254
Db	370 GTCACGCTAAATATGATGAGCGGACCGGACACAGTTTGTCCACATATGCGCGAAGATTCC	429
OY	235 tacattccacacctaatgacctaaagcaagtgtctcagtgccaaatgctgagccagcc	314

Dd	430	TACAAAGGACACTGGAACTACTGTACACAACTCCAGCTGTGCCGGCCCCCTGTATACCACAGTG	489
Oy	315	atggagccttcgcgacagccggaactgtctccagaagagaaagacgcagtgtgttgtagcagc	374
Dd	490	ATTGGCCTTCGAGAGATTGGCCCCCTGCACAACCAAGGAAGCACCGACAGTGGCGTGCAG	549
Oy	375	ccaggcaacttctgatcggtccaggagggga	406
Dd	550	CCGGGAATGTTCTGTGCTGCTGGGCCCTCGA	581
 RESULT 13			
AK027080			
LOCUS	2148 bp	mRNA	PRI 29-SEP-2000
DEFINITION	Homo sapiens CDNA: FLJ23427 fls, clone HRC04788, highly similar to HUMTNFRP Homo sapiens tumor necrosis factor receptor 2 related protein mRNA.		
ACCESSION	AK027080		
VERSION	AK027080.1 GI:10440111		
KEYWORDS	o1lgo capping; fls (Full Insert sequence).		
SOURCE	Homo sapiens primary human renal epithelial cells CDNA to mRNA, clone.lib:HRC clone:HRC04788.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (sites) Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Ohtani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S. NEO human cDNA sequencing project Unpublished (2000)		
TITLE	2 (bases 1 to 2148)		
JOURNAL	Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura.Y. Direct Submission Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)		
COMMENT	NEO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing; Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).		
FEATURES			
source	Location/Qualifiers 1..2148 /organism="Homo sapiens" /db_xref="taxon:9606" /cell_type="primary human renal epithelial cells" /clone="HRC04788" /clone_lib="HRC" /note="cloning vector pME18SFL3" 1..2148 /note="highly similar to HUMTNFRP Homo sapiens tumor necrosis factor receptor 2 related protein mRNA"		
BASE COUNT	462 a 705 c 606 g 375 t		
ORIGIN			
Query Match	6.9% Score 60.8 DB 37 Length 2148;		
Best Local Similarity	51.5% Pred. No. 0.0019;		
Matches 140:	Conservative 0; Mismatches 132; Indels 0; Gaps 0;		
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Dd	333 AAGGAATATCTATGAGCCCGACAGCCGCACTTCCTCTCCCGTCCCGCAGACACATAT	392	
Oy	195 gtgaagagaccttcgcyggaagctgaacgycacagtgltgttaaacccttcgccacgcac	254	

Db 393 GTCCTACCTAATATGATACCCATCCGGACACAGTTTGTGCACATGTGCCAGAAATTC 452

QY 255 tacattgcccactcaatgacctgaagaagtgtctgacgagccaaatggtgcccagcc 314

Db 453 TACACACAGCAGCTGAGACTACCTGACCATGCGAGCTGTGGCCCCCTGTGACCCAGTG 512

QY 315 atggagctgagcgagcggagcgaactgtccagagacagagacgcccgtgtgtgtgagc 374

Db 513 ATGGGCTCGTAGAGAGATTGGCCCCCTGCACAAAGCAAGAAAGCCAGTCCGCTGCCAG 572

QY 375 ccaggccactctgtcatcgtccagagcggga 406

Db 573 CCGGGAATGTTCTGTCTGCTGCTGCGCCCTCGA 604

RESULT 14

HUMTNFR11 2394 bp mRNA PRI 03-SEP-1994

LOCUS Human tumor necrosis factor receptor II (TNFR11) mRNA, complete cds.

ACCESSION M55994.1 GI:339757

VERSION M55994.1 GI:339757

KEYWORDS glycoprotein; nerve growth factor receptor related; transmembrane protein; tumor necrosis factor receptor; tumor necrosis factor receptor II.

SOURCE Human histiocytic lymphoma cell line U937, CDNA to mRNA.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2394)

AUTHORS Kohno,T., Brewer,M.T., Baker,S.L., Schwartz,P.E., King,M.W., Hale,K.R., Squires,C.H., Thompson,R.C. and Vaninice,J.L.

TITLE A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335 (1990)

MEDLINE 91045991

FEATURES

source location/Qualifiers

1. 2394

/organism="Homo sapiens"

/db_xref="taxon:9606"

/cell_line="U937"

/cell_type="histiocytic lymphoma"

93. 158

/gene="TNFR11"

/note="putative"

/product="tumor necrosis factor receptor"

93. 1478

/gene="TNFR11"

/note="603. 611 and 669. 677 glycosylation site; 861. 947 transmembrane domain; 948. 1478 cytoplasmic domain; 159. 860 extracellular domain"

/evidence="experimental"

/product="tumor necrosis factor receptor"

/protein_id="AAA36755.1"

/db_xref="GI:339758"

/translation="MAPVAVMAALAVGLELMAAALPAAVAFTPYAPPGSTGRLRE YDQTAOMCCSKCSGPGHAKVECTKSDIVSCGSESTYTOIAMNWPELISGRSS DOVEIACITREONRITCRPMTCAISKSGECRLCPKRCRGREVARPGITTSIVY CRRCAPTSNITSTSDICRPHOICNVVAIPGNASDAVCTSTSPRMAFGVHLQ PVSTRSQHTQPTPEPSTASTFLPLPGSPGAGTGDFALPVGLIVGTALGLLI IGVNCVIMQVKKPKPLCQREAKVPHLPADKAGTGGPQOHLITAPSSSSLES ASALDRAPTRNDPOAPGVGAAGARASTGSSDPSGSHGQVAVTCIVNVCSSD HSSQSSOASTMTGDISSPSPEKDEQVPEFKSECAFRSOLPETPLTGLSTREKLP LGVPDAGMKPS"

93. 1478

/gene="TNFR11"

159. 1475

/gene="TNFR11"

/note="putative"

/product="tumor necrosis factor receptor"

BASE COUNT 484 a 743 c 739 g 428 t

ORIGIN

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Best Local Similarity 46.9%; Pred. No. 0.0022;

Matches 224; Conservative 0; Mismatches 251; Indels 3; Gaps 1;

QY 164 gtgtgcccactgcaagtcaggtatcgtgtgaagaagcctgcggagctgaagcgg 223

Db 248 GTGCTGAGCAAGATGCTCGCGCGGCCAATGCAAAAGTTCTGTACCAAGACTCGGA 307

QY 224 cacagtgtgaacctgtccctccagacatacatgtccacacttaagtgcctaagca 283

Db 308 CACCGTGTGACTCTCTGTGAGGACAGACATACACCACCTCTGGAAGCTGGTCCGA 367

QY 284 gtgtgcaagtgcacaatgtgtgacccagcagcctgcggcggagcggagcagctgc 343

Db 368 GTGCTTGAGCTGTGG---CTCCCGCTGTAGCTGTGACCAAGTGAAGTCAAGCTTGAC 424

QY 344 caggacagaagacgacgtgtgtgtgagccagagccacttctgcatcgtccagagcgg 403

Db 425 TCGGGAACAGAACCGCATGTGACATGACAGGCGCGCTGTGACTGCGCGCTGAGCAAGCA 484

QY 404 ggaacactgcgcgctgtgcgagcttaagcacaactccagccgggagcagaagtgcaga 463

Db 485 GGAGGGGTGCGCGCTGTGCGCGCGCTGCGCAAGTCCGCGCTTGCGCTGGCCAG 544

QY 464 gggagcaccagagagtcagagacacccctgtgtgagaactgcccggggagcctctcc 523

Db 545 ACCAGGAACAGAACATCAGACAGTGTGTCAGAGCCCTGTGAGCCCGGAGACTTTCGA 604

QY 524 caatggacccttgaggaatgtcagaacacagacaaagtgaagctgtgtgaagaagc 583

Db 605 CACGACTTATCAGAGATTTTGACAGGCCCCACAGACTGTGAAGCTGTGAGCCATCCC 664

QY 584 cggagctggagaccagcagctcccaactggatgtgtgttcttcaggagactgtc 641

Db 665 TGGGAATGCAAGCAGGAGATGACAGTGTGACAGTCCACGTCGCCGCCGAGATGAGCC 722

RESULT 15

LOCUS 136350 691 bp DNA PAT 13-MAY-1997

DEFINITION Sequence 12 from patent US 5606031.

ACCESSION 136350

VERSION 136350.1 GI:2086863

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 691)

AUTHORS Lile,J., Kohno,T., Bonam,D. and Rosendahl,M.S.

TITLE Production and purification of biologically active recombinant neurotrophic protein in bacteria

JOURNAL Patent: US 5606031-A 12 25-FEB-1997;

MEDLINE

FEATURES

source location/Qualifiers

1. 691

/organism="unknown"

BASE COUNT 160 a 198 c 190 g 143 t

ORIGIN

Query Match 6.8%; Score 59.6; DB 81; Length 691;

Best Local Similarity 49.7%; Pred. No. 0.0046;

Matches 180; Conservative 0; Mismatches 179; Indels 3; Gaps 1;

QY 164 gtgtgcccactgcaagtcaggtatcgtgtgaagaagcctgcggagcctgaagcgg 223

Db 228 GTGCTGAGCAAGATGCTCGCGCGGCCAATGCAAAAGTTCTGTACCAAGACTCGGA 287

QY 224 cacagtgtgaacctgtccctccagacatacatgtccacacttaagtgcctaagca 283

Db 288 CACCGTGTGACTCTCTGTGAGGACAGACATACACCACCTCTGGAAGCTGGTCCGA 347

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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(Without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87.3	99.1	1724	5	PCT-US96-12374-1 Sequence 1, Appl
2	59.6	6.8	691	1	US-08-266-080B-12 Sequence 12, Appl
3	59.6	6.8	691	5	PCT-US95-05423-12 Sequence 12, Appl
4	58	6.6	1557	1	US-08-385-229-3 Sequence 3, Appl
5	58	6.6	1641	1	US-08-385-229-1 Sequence 1, Appl
6	58	6.6	1641	2	US-08-650-000-1 Sequence 1, Appl
7	58	6.6	1641	6	5395760-1 Patent No. 5395760
8	57	6.5	1004	4	US-09-071-433-85 Sequence 85, Appl
9	55.8	6.3	519	2	US-08-249-189-4 Sequence 4, Appl
10	55.8	6.3	519	2	US-08-484-624A-4 Sequence 4, Appl
11	55.8	6.3	519	3	US-08-477-733B-4 Sequence 4, Appl
12	55.8	6.3	519	3	US-09-088-913A-4 Sequence 4, Appl
13	47.2	5.4	1600	3	US-08-602-791-1 Sequence 1, Appl
14	46.2	5.2	3796	2	US-08-762-308-11 Sequence 11, Appl
15	46.2	5.2	3813	2	US-08-650-000-3 Sequence 3, Appl
16	46.2	5.2	3813	6	5395760-3 Patent No. 5395760
17	42.2	4.8	1006	4	US-08-911-423-3 Sequence 1, Appl
18	41.8	4.7	1788	1	US-08-225-989-1 Sequence 1, Appl
19	41.8	4.7	1788	1	US-08-570-923-1 Sequence 1, Appl
20	41.8	4.7	1788	1	US-08-580-014-1 Sequence 1, Appl
21	41.8	4.7	1788	4	US-09-079-785-1 Sequence 1, Appl
22	41.8	4.7	3627	2	US-08-232-087A-1 Sequence 1, Appl
23	41.4	4.7	848	1	US-08-192-480A-1 Sequence 1, Appl
24	39.2	4.4	1057	1	US-08-147-784-1 Sequence 1, Appl
25	38.8	4.4	618	1	US-08-097-827-6 Sequence 6, Appl
26	38.8	4.4	618	1	US-08-494-574-6 Sequence 6, Appl
27	38.8	4.4	1317	1	US-08-097-827-10 Sequence 10, Appl

28	38.8	4.4	1317	1	US-08-494-574-10	Sequence 10, Appl
29	38.4	4.4	1464	4	US-09-188-930-255	Sequence 255, Appl
30	38.4	4.4	1633	4	US-09-188-930-73	Sequence 73, Appl
31	37	4.2	1878	3	US-08-996-139-14	Sequence 14, Appl
32	36.4	4.1	759	4	US-09-042-785A-6	Sequence 6, Appl
33	36.4	4.1	1164	2	US-08-794-796-1	Sequence 1, Appl
34	36.4	4.1	1815	4	US-09-042-785A-24	Sequence 24, Appl
35	36.4	4.1	2186	3	US-08-959-382-1	Sequence 1, Appl
36	36.4	4.1	2612	4	US-09-042-785A-23	Sequence 23, Appl
37	36.4	4.1	2638	4	US-09-042-785A-22	Sequence 22, Appl
38	36.2	4.1	1391	3	US-08-896-139-3	Sequence 3, Appl
39	36.2	4.1	3115	3	US-08-896-139-1	Sequence 1, Appl
40	36.2	4.1	3136	3	US-08-996-139-5	Sequence 5, Appl
41	36.2	4.1	3136	4	US-09-435-296-3	Sequence 3, Appl
42	36	4.1	1719	4	US-09-042-785A-5	Sequence 5, Appl
43	36	4.1	3331	4	US-09-042-785A-1	Sequence 1, Appl
44	36	4.1	18318	1	US-08-414-926A-6	Sequence 6, Appl
45	36	4.1	18318	2	US-08-926-922-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
PCT-US96-12374-1
Sequence 1, Application PC/TUS9612374
GENERAL INFORMATION:
APPLICANT: Northwestern University
TITLE OF INVENTION: Herpes Virus Entry Mediator
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESS: Dressler, Goldsmith, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12374
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Northrup, Thomas E.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: NOR3446P020PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5400
TELEFAX: (312) 616-5460
TELEX: --
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1724 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 294..1145
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 294..1142
PCT-US96-12374-1
Query Match 99.1%; Score 873; DB 5; Length 1724;
Best local Similarity 99.4%; Pred. No. 3.2e-228;

Matches 876; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 cctgagacatgagacccctctgagagctgagagcctctcctctgagatcaccccaagaa 60
   |||||
Db 286 CCGAGGACATGAGACCTCTGAGAGACTGGGGGCTCTCTCTGAGATCCACCCCGAGAA 345
QY 61 ccgagctctgagagctgagctglatctacactctcctgagagcccccgtacgcccag 120
   |||||
Db 346 CCGAGCTCTGAGAGCTGCTGATCTCACTCTCTGGAGGCCCTGCTAGGCCCGAG 405
QY 121 cctgcccctctcagagagagagagagagagagagagagagagagagagagagag 180
   |||||
Db 406 CTTGCGCTCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
QY 181 gtcacagatctgctgaaagagagagagagagagagagagagagagagagagagag 240
   |||||
Db 466 GTCCAGGTTATCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 525
QY 241 gccctcagagacactatctgacacactcaatgagcctaagagagagagagagagag 300
   |||||
Db 526 GCCCTCAGAGACCTACATGATGCGCACCTCAATGAGCCTAAGCAAGTGTCTGAGCCAA 585
QY 301 tctgtgagacagagagagagagagagagagagagagagagagagagagagagag 360
   |||||
Db 586 TGTGTGACCCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 645
QY 361 tctgtgagacagagagagagagagagagagagagagagagagagagagagagag 420
   |||||
Db 646 TGTGTGCTGACAGCCAGGCACTTCTGATCTGATCTGATCTGATCTGATCTGATCT 705
QY 421 gccgcgcttacgacacactcagagagagagagagagagagagagagagagagagag 480
   |||||
Db 706 GCGCGCTTACGCGACACTCCAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 765
QY 481 aggaacacccctgtctgagaatgcccccgagagagagagagagagagagagagag 540
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Db 766 AGGACACCCCTGTGTGAGAACTGCCCCCGGGGAGACTTCTCTCCAAATGAGACCTG 825
QY 541 aatgtacagacagagagagagagagagagagagagagagagagagagagagagag 600
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Db 826 AATGTACAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 885
QY 601 gctcccaactgagatggtgttctctcagagagagagagagagagagagagagagag 660
   |||||
Db 886 GCTCCACAGTGTGATGTGTGTCTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 945
QY 661 cagtgtgagacatcatatgtgtgaaagagagagagagagagagagagagagagag 720
   |||||
Db 946 CAGTTGGCCCTAAATCATATGTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1005
QY 721 tctgtccctcagagagagagagagagagagagagagagagagagagagagagagag 780
   |||||
Db 1006 TCGTCTCCGCTCCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1065
QY 781 tgcagagccctcagagagagagagagagagagagagagagagagagagagagagag 840
   |||||
Db 1066 TCGAGGCGCCCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1125
QY 841 ggaagagagagagagagagagagagagagagagagagagagagagagagagagag 881
   |||||
Db 1126 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1166

```

RESULT: 2

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US-08-266-080B-12
; Sequence 12, Application US/08266080B
; Patent No. 5606031
; GENERAL INFORMATION:
; APPLICANT: Jack Lille
; APPLICANT: Tadahiko Kohno
; APPLICANT: Duane Bonam
; APPLICANT: Mary S. Rosendahl
; TITLE OF INVENTION: Production of Biologically Active

```

```

; TITLE OF INVENTION: Recombinant Neurotrophic Protein
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/266,080B
; FILING DATE: 27-JUNE-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/240,122
; FILING DATE: 09-MAY-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/087,912
; FILING DATE: 06-JULY-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/680,681
; FILING DATE: 04-APRIL-1991
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/594,126
; FILING DATE: 09-OCT-1990
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/547,750
; FILING DATE: 02-JULY-1990
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/505,441
; FILING DATE: 06-APRIL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: SYNE200C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 691 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
US-08-266-080B-12

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Query Match 6.8%; Score 59.6; DB 1; Length 691;
Best Local Similarity 49.7%; Pred. No. 2.4e-07;
Matches 180; Conservative 0; Mismatches 179; Indels 3; Gaps 1;

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QY 164 gtagtcccccaatgtagcagagagagagagagagagagagagagagagagagagag 223
   |||||
Db 228 GTGCTCAGACAGAGCTCTCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 287
QY 224 caagatgtgtgaacccctgcccctcagagagagagagagagagagagagagagagag 283
   |||||
Db 288 CACCGTGTGTGACTCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 347
QY 284 gtagtgcagagagagagagagagagagagagagagagagagagagagagagagag 343
   |||||
Db 348 GTGCTTGAGCTGTGG---CTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 404
QY 344 cagagagagagagagagagagagagagagagagagagagagagagagagagagagag 403
   |||||
Db 405 TCGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 464
QY 404 ggaacacctgcgcgcgctgagagagagagagagagagagagagagagagagagagag 463
   |||||

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[illegible]

RESULT 3
PCT-US95-05423-12

```

Sequence 12, Application PC/YUS9505423
GENERAL INFORMATION:
APPLICANT: Jack Lille
APPLICANT: Tadshiko khono
APPLICANT: Duane Bonam
APPLICANT: Mary S. Rosendahl
TITLE OF INVENTION: Production of Biologically Active
TITLE OF INVENTION: Recombinant Neurotrophic Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 Inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05423
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/266,090
FILING DATE: 27-JUNE-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,122
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/680,681
FILING DATE: 04-APRIL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/505,441
FILING DATE: 06-APRIL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: SYNE200/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 691 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-05423-12

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Query Match	6.8%	Score 59.6;	DB 5;	Length 691;
Best Local Similarity	49.7%	Pred. No. 2.4e-07;		
Matches 180; Conservative	0;	Mismatches 179;	Indels 3;	Gaps 1

OY	164	gtctcccccagaatgacagtcagtcacaggttacgtgtgaagaagcgctcgaggggagacgtacagcg	222
Db	228	gtctgcacgacgaagtccttcggccggccacacatgacaaatcttctgtgtaccanagaccttgga	28
OY	224	cacagttgtgaacctgccttcgccaccaggaacctatattgcccacctcatatgacctaaagca	283
Db	288	cacgctgtgtgactcctctgtgaggaagacacatataccacgtcttgaaactgtgggttccga	344
OY	284	gtgtctgcagttgccaaatgtgtgacccagccatgtgacctgcgctcgagccggaaactgtc	343
Db	348	gtgctgtgagctgtg ---ctcccgctgtgagctgtgacacaggtgaaactgaagctctcac	404
OY	344	cagagcagaagaagcgcgtgtgtgttgagcccaaggccactctgtacatgtgtccagagcgg	403
Db	405	tgcggaaacagaaacgcacatcttcacactgcagccggcctgtgactgcgccttgacgaacga	464
OY	404	ggaacacatgcgcggtgtgcgcgttcaacgcacctccagcccggtgcagagtgltcgaa	463
Db	465	ggagggggtgcggcgtgtccggccgcgtgcgaataatgcccggccttccggcgtggccag	524
OY	464	ggagagcaaccgaagtcaggaacacctgtgtcagaatgcccccggggagacctcttc	523
Db	525	accaggaactgaataacatcagacgtgtgtgcacacccctgtgccccggggagcttccaa	584
OY	524	ca 525	
Db	585	ca 586	

RESULT 4
US-08-385-229-3

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RESULT 6
US-08-650-000-1
Sequence 1, Application US/08650000
Patent No. 5945397
GENERAL INFORMATION:
APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
City: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,000
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/468,453
FILING DATE:
APPLICATION NUMBER: US/08/038,765
FILING DATE:
APPLICATION NUMBER: US 421,417
FILING DATE:
APPLICATION NUMBER: US 405,370
FILING DATE: 11-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 421,417
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,635
FILING DATE: 10-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wright, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2501-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1641 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Fibroblast
CELL LINE: WI-26 V44
IMMEDIATE SOURCE:
LIBRARY: WI-26 V44
CLONE: 1
FEATURE:
NAME/KEY: CDS
LOCATION: 88..1473
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 154..1470
FEATURE:

```

NAME/KEY: sig-peptide
LOCATION: 88..153
PUBLICATION INFORMATION:
AUTHORS: Smith, Craig A.
AUTHORS: Davis, Terri
AUTHORS: Anderson, Dirk
AUTHORS: Solam, Lisabeth
AUTHORS: Beckmann, M. P.
AUTHORS: Jerzy, Rita
AUTHORS: Dower, Steven K.
AUTHORS: Cosman, David
AUTHORS: Goodwin, Raymond G.
TITLE: A Receptor for Tumor Necrosis Factor Defines
TITLE: an Unusual Family of Cellular and Viral Proteins
JOURNAL: Science
VOLUME: 248
PAGES: 1019-1023
DATE: 25-MAY-1990

Query Match	6.68;	Score 58;	DB 2;	Length 1641;
Best Local Similarity	49.48;	Pred. No. 8.8e-07;		
Matches 179;	Conservative	0;	Mismatches 180;	Indels 3;
				Gaps 1;

[illegible]

```

RESULT 7
5395760-1
Patent No. 5395760
APPLICANT: SMITH, CRAIG A.; GOODWIN, RAYMOND G.; BECKMANN,
M. PATRICIA
TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
B-RECEPTORS
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/523,635
FILING DATE: 10-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 421,417
FILING DATE: 13-OCT-1989
APPLICATION NUMBER: 405,370
FILING DATE: 11-SEP-1989
APPLICATION NUMBER: 403,241
FILING DATE: 05-SEP-1989
SEQ ID NO:1:

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LENGTH: 1641
5395760-1

Query Match 6.6%; Score 58; DB 6; Length 1641;
Best Local Similarity 49.4%; Pred. No. 8.8e-07;
Matches 179; Conservative 0; Mismatches 180; Indels 3; Gaps 1;

OY 164 gtctgcggcccaagtgcagtcagttatctgtgtgaaggaagcctgcggggaagtcgaaggg 223
DB 243 gtctgtgaagcaaatgtcgcgggccaacatgcaaaagttcttctgtacccaagcctcgga 302
OY 224 cacagtggtgaacccctgcctccagccactacattgcccactcaatgtgccaagcaa 283
DB 303 caccgtgtgtgactcctgtgtgaagacacataaccagctctgtgaacgtggtccgga 362
OY 284 gtctgtgcaagtcgcaaatgtgtgaacacagcattggtcctgcggcggaagccgaactgtc 343
DB 363 gtgctt---gagctgtgtgctcccgctgtgactgtgaccaggtgaaactcaagcctgcac 419
OY 344 caggacagagaagccgctgtgtgtgtgacagccagagccacttctgcatctgcaagacgg 403
DB 420 tcgggaacagaacccgactgtgacactgtgacagcccgctgtgactgcgctgaggaagca 479
OY 404 ggaacactgtgcgcgctgtgccgcttaccgcaacctccagccggcggaaggtgcagaa 463
DB 480 ggaagggtgtgcggctgtgtgcgcgcgcgcgaagtgtgcgcggcgtctgcgtgtgccaag 539
OY 464 ggaagacacgagatgtaagacaacctgtgtgaactgcccccgagggaacttctcc 523
DB 540 accaggaactgaaacatcagacgtgtgtgcaagccctgtgcccgaggagcttccaa 599
OY 524 ca 525
DB 600 ca 601

RESULT 8

US-09-071-433-85
; Sequence 85, Application US/09071433A
; Patent No. 6197584
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Cowsett, Lex M
; TITLE OF INVENTION: Antisense Modulation of CD40 Expression
; FILE REFERENCE: RTS-0002
; CURRENT APPLICATION NUMBER: US/09/071,433A
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 1004
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-071-433-85

Query Match 6.5%; Score 57; DB 4; Length 1004;
Best Local Similarity 47.8%; Pred. No. 1.4e-06;
Matches 205; Conservative 0; Mismatches 215; Indels 9; Gaps 1;

OY 92 ctctccgtgagagccctctgtaagcccccagctctgcgcgtctctgaaggaagagagaccc 151
DB 83 ctgtctgtgagcagcgtgtcatcacaacacccactgtgacagagaanaaaagtaact 142
OY 152 agtgggtcgcagtgctgcccacaagtgcaggttaccgtgtgaaggagggcctggcg 211
DB 143 aataaacagtcagtgctgttcttctgtgccagcagacagaacatggtgtgactgtcac 202
OY 212 ggaagctgaagggacagtggtgtgaacccctgcccacaggaacctaatgtccacctcaa 271

DB 203 agagttcactgaaacgaatgtccttcttcgtggtgaaaggaattccttagaacctcgaa 262
OY 272 tggcctaagcaatgtctgtcagtgccaatgtgtgacccaagcattggcctggcgag 331
DB 263 cagagagacacactgtccaccagcacacaatacttgcaccccaactgaggtcttgggttcaa 322
OY 332 ccggaactgtccaggaacagaacgcggtgtgtgtgtgaagccagccgaacttcgaat 391
DB 323 gcagaagggactctcgaagaacacacatctgcacctgtgaagaagagctgtgactgtac 382
OY 392 cgtccagagcggggaacactgcgcgctgtgcgcgttaccgccaacctcagcccgagca 451
DB 383 gagtggagcctgtgagagctgtgtctctgcacccgtcatgtctc-----gcccgctt 433
OY 452 gagggtgcgaagaggggcgacccgagagtgcaagacacctgtgtcagaactgtcccccgg 511
DB 434 tgggttcaagcgaattgtcacaagggttctctgataccactgtgagccctgcccagtcgg 493
OY 512 gacctctc 520
DB 494 ctctctctc 502

RESULT 9

US-08-249-189-4
; Sequence 4, Application US/08249189
; Patent No. 5961974
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,189
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 519 base pairs


```

RESULT 11
US-08-477-733B-4
: Sequence 4, Application US/08477733B
: Patent No. 59817724
: GENERAL INFORMATION:
: APPLICANT: ARMITAGE, RICHARD
: APPLICANT: FANSLLOW, WILLIAM
: APPLICANT: SPRIGGS, MELANIE
: APPLICANT: SRINIVASAN, SUBHASHINI
: APPLICANT: GIBSON, MARYLOU
: APPLICANT: MORRIS, ARVIA E.
: APPLICANT: MCGREW, JEFFREY
: TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: IMMUNEX CORPORATION
: STREET: 51 UNIVERSITY STREET
: CITY: SEATTLE
: STATE: WASHINGTON
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/477,733B
: FILING DATE: June 07, 1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/249,189
: FILING DATE: May 24, 1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/969,703
: FILING DATE: October 23, 1992
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/805,723
: FILING DATE: December 5, 1991
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/783,707
: FILING DATE: October 25, 1991
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia A.
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2802-D
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 2065870430
: TELEFAX: 2065870606
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 519 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: HUMAN
: IMMEDIATE SOURCE:
: CLONE: CD40 EXTRACELLULAR REGION
: US-08-477-733B-4

```

```

Matches 190; Conservative 0; Mismatches 192; Indels 9; Gaps 1
QY 130 cctgcagaaggaagcagagtaaccagatggtggtctccgagatgtctgtcccaatgagtcagtt 189
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Db 16 CATGCAGAGAAAACAGTAACTAAATAAACAGTCAGTGTGCTTTGTGTCACGCGAGAC 75
QY 150 atcgtgtgaagaagccttcgagagagctgtacgagcagacagtgtgtgaacctgtccctcag 249
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 76 AGAAACTGGTGTAGTACTGTGCACACAGAGTTCTACTGAAACGGAAATGCTTCTTCGGGTGAAA 135
QY 250 gcacctaatatgtcccaactcctaattgacctaaagcaagtgtctgtcagatgtgcacaatgttgacc 309
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 136 GCGAATTCTTGATACACACTGGAAACAGAGACACACTGCCACACAGCAAAATCTCGAAC 195
QY 310 cagcacaatgggctcgcgcgagcgcggaactgtctccagaacagagaagacgcgtgtgtgtt 369
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 196 CCAACTTAGGGGCTTGGGGTCCAGCGAAGGGGCTCAGAAACACAGACCAATCTCCACT 255
QY 370 gcagccaggagccactctgtcatctgtccagagagagagaccactgtgcccgtgtgcgcgctt 429
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 256 GGAAGAAGAGGCTGCGACATGTACAGTGAAGGCTGTGAAGCTGTCTCCGACCCCTAT 315
QY 430 acgcgaactccagcccgagccagaggtgcagaaaggagagacagagatcaagacacc 489
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 316 GCTC-----GCCCGGCTTTGGGGGTCAAGCAATTTGTACAGGGGTCTGTGTACCA 366
QY 490 tgtgtcagaactgcgccccgggagacctctc 520
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 367 TCTGCGAGCCCTGCCCACTGCGCTTCTTCTC 397

RESULT 12
US-09-088-913A-4
; Sequence 4, Application US/0908913A
; Patent No. 6087329
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; APPLICANT: MORRIS, ARVIA E.
; APPLICANT: MCGREW, JEFFERY
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,913A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,624
; FILING DATE:
; APPLICATION NUMBER: 08/477,733
; FILING DATE: June 07, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; PRIOR APPLICATION DATA:

```


CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,308
FILING DATE: 09-DEC-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/224,593
FILING DATE: 05-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kilchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTS-335--1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 418-3000
TELEFAX: 474-7577
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3796 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-762-308-11

Query Match 5.2%; Score 46.2; DB 2; Length 3796;
Best Local Similarity 48.1%; Pred. No. 0.0019;
Matches 194; Conservative 0; Mismatches 203; Indels 6; Gaps 2;

QY 126 ccgtccgcgaaggaagcaggtaccagctggtccgagctgcgcacgaagtgcaccca 165
DB 163 CAGATCTCACAGGAATATCTATGACAGGAAGGCTCAGATGCTGCTAGTCTCTCT 222
QY 186 ggtatcgtgtgaaggaagcgtcgaggaagcgtgacgaagtggtgaacctgcctc 245
DB 223 GGGCAATATGTGAACATTTCTGCAACAAGACCTCGACACCGTGTGCGGACTGTGAG 282
QY 246 ccaggaacctacattgcacacctcaatgagcctaagaagtgtctgcaagtgcacaa 305
DB 283 GCAAGCATGTATATCCAGAGTCTGGAACCACTTTCGTACATGTTTGAAGCTGC--AGTTC 339
QY 306 gaccacagcctatggtcgtcgagcgcgagccggaactgtctccagagaagacgcctgt 365
DB 340 TCTGTATACACTAGCAGGATGAGATCCGGCTGCACCTAAGACGACGAGTGTGT 399
QY 366 ggttcgagccagcagcactctcatcgtccaggaagcgtg--gaccactgcgcgcgtgc 422
DB 400 GCTTGGCAAGCTGCGAGTACTGCGCTTGAACCACTTCTGACACTTCCACACTGC 459
QY 423 cgcgcttaagcgaacctccagccgagcgaaggtgcaagaaggaagcagcagagtcag 482
DB 460 ATGAGGCTGAGCAAGTGGCGCTTGGAGTGGCCAGTTCAGAGCCCAATGGA 519
QY 483 gacacccctgtgtcagaactgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 525
DB 520 AATGTGCTATGCAAGGCTGTGCTGCCAGGAGCGTCTCTGACA 562

RESULT 15
US-08-650-000-3
Sequence 3, Application US/08650000
Patent No. 5945397
GENERAL INFORMATION:

APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,000
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US/08/468,453
FILING DATE:
APPLICATION NUMBER: US/08/038,765
FILING DATE:
APPLICATION NUMBER: US 403,241
FILING DATE: 05-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 405,370
FILING DATE: 11-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 421,417
FILING DATE: 13-OCT-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,635
FILING DATE: 10-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wright, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2501-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: mouse
STRAIN: C57BL/6
CELL TYPE: T-helper cell
CELL LINE: 7B9
IMMEDIATE SOURCE:
CLONE: 11

FEATURE:
NAME/KEY: CDS
LOCATION: 55..1479
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 121..1476
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 55..120
US-08-650-000-3

Query Match 5.2%; Score 46.2; DB 2; Length 3813;

Best Local Similarity 48.1%; Pred. No. 0.0019;
Matches 194; Conservative 0; Mismatches 203; Indels 6; Gaps 2;

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QY 126 ccgctcgtcaaggaggaagataccagtggtccgagtgctgcccgaagtgcagtcoca 185
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Db 175 CAGATCTTCACAGGAATCTATGACAGGAAGGCTCAGATGTCTGTCTAAGTGTCTCTCT 234
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QY 186 ggttcacgtgtgaaggagggcctgcgggagcgtgacgggacagtgltgaaacctgacct 245
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Db 235 GGCCAAATATGTGAACAATTTCTGCAACAAGACTCGGACACCGTGTGTGCGGACTGTGAG 294
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 246 ccaggcaacctacaltgcccacctcaaltgacctgaagcaagtgctgcagtgccaaatglt 305
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 295 GCAAGCATGTATACCCAGAGTCTGGAACCAAGTTTGTACATGTGTGAGCTGC---AGTTCT 351
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QY 306 gaccacagccatgggcctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 365
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Db 352 TCCGTGTACCACTGACACAGGTGAGATCCGCGCTGCACTAAACAGACAGAACCGAGTGTGT 411
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QY 366 ggttgcaagcccaaggccaactctgtcatcgtgccaggaagcgg---gaaccactggccgcgtgc 422
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Db 412 GCTTGCGAAGCTGGCAGGTACTGCGCCTTGAAACCAATTTCTGCGAGCTGTGACAGTGC 471
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QY 423 cgcgccttaagccaacctccagccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 482
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 472 ATGAGGCTGAGCAAGTGGCGCCTGCGCTTCGAGTGGCGAGTTCAGAGAGCCCAATGGA 531
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QY 483 gacacccctgtgtcgaactgccccccgggggaacctctctccca 525
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Db 532 AATGTGCTATGCAAGGCTGTGCCCCAGGGACGTTCTCTGACA 574
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Search completed: April 24, 2001, 18:41:23
Job time: 12235 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd..

OM nucleic - nucleic search, using sw model

Run on: April 24, 2001, 17:12:21 ; Search time 1027.86 Seconds
(without alignments)
6006.262 Million cell updates/sec

Title: US-08-741-095b-25

Perfect score: 881

Sequence: 1 cctgagcatggagcctcct.....ccacagactlgcaccccca 881

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 segs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_est4:*

5: gb_est5:*

6: gb_est6:*

7: gb_est7:*

8: gb_est8:*

9: gb_est9:*

10: gb_est10:*

11: gb_est11:*

12: gb_est12:*

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14: gb_est14:*

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 189: em_estp88:*

190: gb_gss25:*
 191: gb_gss26:*
 192: gb_gss27:*
 193: gb_gss28:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	453	51.4	493	93	AM630737
2	400.2	45.4	796	135	BE728963
3	376.8	42.8	523	137	BE891768
4	348.6	39.6	589	1	AA020847
5	311.4	35.3	532	89	AM72968
6	281.2	31.9	428	4	AA262421
7	271	30.8	457	1	AA021617
8	267	30.3	823	19	AI356409
9	244	27.7	482	107	BE386504
10	240	27.2	556	8	AA481843
11	228.8	26.0	251	7	AA426526
12	218.6	24.8	719	21	AI479005
13	213.6	24.2	426	2	AA088363
14	211.4	24.0	237	111	BE699740
15	203.2	23.1	682	97	AM978536
16	203.2	23.1	304	4	AA293583
17	194.2	22.0	262	135	BE770179
18	187	21.2	274	147	BE676441
19	178.8	20.3	672	111	BE676441
20	176	20.0	627	108	BE465035
21	153	17.4	892	13	AA890591
22	151	17.1	565	24	AI765809
23	148	16.8	606	92	AM590114
24	146.4	16.6	506	1	AA018179
25	139.4	15.8	641	13	AA934011
26	127.8	14.5	597	92	AM590183
27	124.4	14.1	597	105	BE221308
28	119.8	13.6	510	11	AA722732
29	76.4	8.7	560	105	BE234440
30	75.2	8.5	449	14	AA987435
31	71.8	8.1	191	1	AA015831
32	70	7.9	520	27	AI989788
33	69.6	7.9	581	25	AI794181
34	60.2	6.8	375	133	BE014983
35	57	6.5	595	137	BE908916
36	55.8	6.3	484	142	N25156
37	55.4	6.3	576	93	AM657964
38	55.4	6.3	871	3	AA203290
39	53.8	6.1	576	106	BE285979
40	53.8	6.1	639	107	BE375846
41	53.8	6.1	679	3	AA207651
42	52.4	5.9	821	16	AI119599
43	52.2	5.9	500	38	AM012145
44	52.2	5.9	732	87	AM211419
45	51.6	5.9	393	97	AM934924

ALIGNMENTS

RESULT 1
 AM630737
 LOCUS
 DEFINITION
 AM630737 493 bp mRNA
 hb86h04.y1 NCI-CCAP-GUI Homo sapiens cDNA clone IMAGE:2969719 5'
 similar to TR:Q92956 Q92956 HERPESVIRUS ENTRY MEDIATOR. ;, mRNA
 sequence.
 AM630737
 VERSION
 AM630737.1 GI:7377527
 EST
 31-MAR-2000
 5'

Source	Organism	Human
REFERENCE	1 (bases 1 to 493)	
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: Chris Mokaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/TLNL at: image.lnl.gov/image/html/lresources.shtml Seq primer: -40RP from Glbco High quality sequence stop: 400. Location/Qualifiers 1..493 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2969719" /clone_id="NCI_CGAP_G01" /tissue_type="2: pooled high-grade transitional cell tumors" /lab_host="DH10B" /note="Organ: genitourinary tract; Vector: pCMV-SPORT3; Site_1: Salt; Site_2: NCI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies.." BASE COUNT 112 a 144 c 156 g 81 t ORIGIN	
Query Match	51.4%; Score 453; DB 93; Length 493;	
Best Local Similarity	94.9%; Pred. No. 8.6e-104;	
Matches 468; Conservative	0; Mismatches 25; Indels 0; Gaps 0;	
Db 1	GTGTGGTGTGCAGCCCGACGCTTCTGTGATGTGCAGACGCGGACCTCTCGCGCGCTG	60
422	ccggagcttagcgcacccctccaccccgggcgaagaggtgaagaaggagacacccgagatca	481
61	CCGGGCTTACCCCACTCCACCCCGGCGCAAGGGTGCAAGAGGAGGACCGAGAGTCA	120
482	ggacacctgtgtcagaactgcccccggggagacctctctccaatggagacctgtgaaga	541
121	GGACACCCCTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCCATGGGACCTTGAAGA	180
542	atgtcagacaccagaccaaagtgcagtgtgtgtgaagaaagccggagcttggacacag	601
181	ATGTACAGACCAAGCAAGTGCACCTGCTGTGACGACGAAGCCGGAGCTGGAGACAG	240
602	ctccacatgggtatgggtgttctctcaaggagaccttgtcatcgtcatctgttctcac	661
241	CTCCACAGGGGTATGGTGTCTCTCGAGGAGCCTCTCATTCGTCATTTGTGCTCAC	300
662	agttggacctatcatatgtgtgaagaagaagaagccaaagggtgagtgaagcaagtgat	721
301	AGTTGGCTATTCATATGTGTGCAAAAAGAAAGCAAGGAGGAGGTGATGTAGTCAAGTAT	360
722	cgctccgtctcagcaggaaagacagagagcagaaagtgtgaagccacagtcatttgaagccct	781
361	CGTCTCCCGCCAGCGGAAAGACAGAGAGGAGAGGTGAGGCCACAGTCATTGAGAGGCC	420
782	gcgaagccctcgcgaagctcaccacggtggccgttgaggagaacaataacctcattcaagg	841

Db	421	TCGACCCCTCCCGACGTACACCAAGGAGGAGCCATGAGACATATACCGTATTCACGGG	480
QY	842	gaggagcccaaac 854	
Db	481	GAGAACCGCGAACC 493	
RESULT	2		
LOCUS	BE728963	796 bp	EST
DEFINITION	601562209p1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831818 5',		15-SEP-2000
ACCESSION	BE728963		
VERSION	BE728963.1	GI:10142955	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 796)		
JOURNAL	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Tel: (301) 496-1550		
	Email: Robert.Strausberg@nih.gov		
	Tissue Procurement: ATCC/DCTD/DTF		
	cDNA Library Preparation: Ling Hong/Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov		
	Plate: L1CWM508 row: a column: 03		
	High quality sequence start: 10		
	High quality sequence stop: 681.		
FEATURES			
source	location/Qualifiers		
	1..796		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:3831818"		
	/clone_1ib="NIH.MGC.20"		
	/tissue_type="melanotic melanoma"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: skin; Vector: pORF7; Site_1: XhoI; Site_2:		
	EcoRI; cDNA made by oligo-dt priming. Directionally		
	cloned into EcoRI/XhoI sites using the following 5'		
	adaptor: GGCACGAG(G). Size-selected >500bp for average		
	insert size 1.8kb. Library constructed by Ling Hong in		
	the laboratory of Gerald M. Rubin (University of		
	California, Berkeley) using ZAP-cDNA synthesis kit		
	(Stratagene) and Superscript II RT (Life Technologies)."		
BASE COUNT	135 a 267 c 234 g 160 t		
ORIGIN			
Query Match	45.4%; Score 400.2; DB 135; Length 796;		
Best Local Similarity	91.9%; Pred. No. 1.8e-90;		
Matches 501; Conservative	0; Mismatches 33; Indels 11; Gaps 7;		
QY	1	cctgaggaatgagactctctgagagcttggggcctctccctggagatcaccacaga	60
Db	237	CCTGAGGATGAGAGCTCTCTGAGAGCTGGGGCCCTCTCCCTGGAGATCCACCCAGAA	296
QY	61	ccgaagcttgaagctgtgtctatctcaactctctgagagccctgactagcccca	120
Db	297	CCGAGCTTTGAGAGCTGGTGTCTGATATCTACCTTCTTGAGAGCCCCCTCTAGCCCCAG	356
QY	121	ctctgcgctctctgcaagagagagtaaccacagtgagctcgcagatgtctgccccaa	180
Db	357	CTCTGCGCTCTCTGCAAGAGAGGACGAGTACCCAGTGGGCTCCGAGTGTGCCCCAAGTGA	416
QY	181	gtccaagttatctgtgtgaagagagccctgcgggagagctgaagggacacgtgtgtga	240

Query Match	42.88;	Score 376.8;	DB 137;	Length 523;
Best Local Similarity	98.18;	Pred No. 1.3e-84;		

[illegible]

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/clone="IMAGE:363721"
/clone_lib="Soares retina N2b4HR"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/Note="Organ: eye; Vector: pRT3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTACCAATCTGAGTGGAGGCGCGCGCTTTTCTTTTCTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT3 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(A)+ RNA was extracted 6
hrs after their removal. The retina RNA was kindly
provided by Roderick R. McInnes M.D. Ph.D. from the
University of Toronto. Library constructed by Bento
Soares and M. Fatima Bonaldo."

```

```

BASE COUNT      117 a      182 c      183 g      104 t      3 others
ORIGIN
Query Match      39.6%; Score 348.6; DB 1; Length 589;
Best Local Similarity 94.1%; Pred. No. 1.7e-77;
Matches 449; Conservative 0; Mismatches 19; Indels 9; Gaps 8;

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OY 7 gcatgagacccctgagagactgaggcgctcctcctgagatcaccccgagacgagc 66
    |||||||
Db 107 GGATGGACCCCTCTGGAACATGGGGGCTCTCTCCCTGGAGATCCACCCCAAAACCGACG 166
OY 67 tcttgaagctggtcgtatctcaacctctcctgagagacccctgtaagcccaagctcgc 126
    |||||||
Db 167 TCTTGAGGCTGTGTGTATCTCACTTCTGGAAGCCCCCTGTAGCCCCCAGCTCTGC 226
OY 127 cgtcctgcaagagagagagatcaccagtgaggctcagagtgctgcccgaagtgc-a 185
    |||||||
Db 227 CGTCTGCAAGAGAGACAGTACCCAGTGGGCTCCGAGTCTGCCCAAGTCANMTCGA 286
OY 186 ggtatcgttggaagagagcctcgtcgagg-a-gctgaagcgagacagtgtgttaaccc 243
    |||||||
Db 287 GGTATCTGTGGAAGGAGGCTGTGGGGAGACTGACCGGACAGTGTGTAACCCCTGCC 346
OY 244 ctcc-aggcacctaatgcccacctcaatgagcctaaagtgctcagtgccaatg 302
    |||||||
Db 347 CTCAAGGCACTTACATTTGCCCACTCAATGAGCTTAAGCAAGTGTCTCAATGCCAATG 406
OY 303 tctgacccagcagctgagcctgcgcgagccgagactgctccagagacagagacgcgtg 362
    |||||||
Db 407 TGTGACCCAGCCATGTGGGCTGTGGGCGAG -CGGAAGTCTCTCAGAGACAGAACGCCGTG 465
OY 363 tctggttgagacccagcagcactctgcatcgtccaagaagggagacactgcccgtgc 422
    |||||||
Db 466 TGTGCTGTCAAC-CCAGGCGCACTTCTGCAATGCT-CAAGAAAGGGAGAACATGTGGCGCGCTGC 523
OY 423 cgcgccttaccacacctcagcccgagagaggttgcaagaagggagagagacagagagt 479
    |||||||
Db 524 CG-GCTTAAGCAACTTCAAGCCCGGG -CAAAAGTGTGCAAGAGGAGAACAGCAAGAGAGT 578

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RESULT 5
LOCUS AM372968 532 bp mRNA EST 04-FEB-2000
DEFINITION OY3-PT0382-171299-043-g07 BT0382 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM372968
VERSION AM372968.1 GI:6877622
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 532)
AUTHORS HGCP http://www.ludwig.org.br/ORESTES.

```

```

TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
CONTACT Simpson A.J.G.
COMMENT Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

```

```

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=OY3&t2=OY3-BT0382-
171299-043-g07&t3=1999-12-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 532.
Location/Qualifiers

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FEATURES
source
1..532
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0382"
/dev_stage="Adult"

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/Note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT      108 a      155 c      182 g      87 t
ORIGIN

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```

Query Match      35.3%; Score 311.4; DB 89; Length 532;
Best Local Similarity 98.1%; Pred. No. 3.8e-68;
Matches 315; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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OY 1 cctgaagcatagagacccctcctgagagactgaggcgctcctcctgagatcaccccgagaa 60
    |||||||
Db 402 CCTGAGCATAGGACCTCTCTGGAAGCTGGGGGCTCTTACTTGGAGATCCACCCCGAGAA 343
OY 61 ccgacgctctgagagctggtcgtatctcaacctctcctgaggagccctgtacgcccag 120
    |||||||
Db 342 CCGAGCTTTGAGGCTGTGTATCTCACTTCCGGAAGCCCCCTGTAGSCCCAG 283
OY 121 cctgcgctcctgcaagagagacagatcaccagtgaggctccagtgctgcccgaagtgc 180
    |||||||
Db 282 CTCTGCCGTCTGCAAGAGAGAGACAGTACCCAGTGGGCTCCGAGTCTGCCCAAGTGA 223
OY 181 gtccaggtatcgtgttaagagagcctgcgggagagctgagcagggagacagtgtggaacct 240
    |||||||
Db 222 GTCCAGGTTATCTGTGAAGAGGCTGTGGGGAGCTGTGAGCGCACAGTGTGAACCTT 163
OY 241 gccctcagagacattacattgcccacacctcaatgcccctcaagcaagtgtcgtgagtgccaaa 300
    |||||||
Db 162 GCCCTCAGGCACTTACATTTGCCCACTCAATGSCCTTAAGCAAGTGTCTGCAAGTCCAAA 103
OY 301 tctgtgacccagccatgagcc 321
    |||||||
Db 102 TGTGTACCCAGGTAAAGAGGC 82

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RESULT 6
LOCUS AA262421 428 bp mRNA EST 13-AUG-1997
DEFINITION ZS17604.r1 NCI-GCB1 Homo sapiens cDNA clone IMAGE:685470 5'
similar to TR:G1167929 G1167929 ORF U144.1; mRNA sequence.
ACCESSION AA262421
VERSION AA262421.1 GI:1897917
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

```

REFERENCE 1 (bases 1 to 428)
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITLE NCI-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 COMMENT Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov

This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 1528 Std Error: 0.00
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 405.

FEATURES

Source
 1..428
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 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /note="Vector: pRT3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, 19D-),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CEBR). cDNA synthesis was
 primed with a Not I - oligo(dt) primer
 [5'-TGTACCAATCTGAAGTGGAGCGGCGCTTCTCCCTGAGATCCACCCCAAGAACGACG
 15'-TGTACCAATCTGAAGTGGAGCGGCGCTTCTCCCTGAGATCCACCCCAAGAACGACG
 1. Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pRT3D vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 78 a 141 c 128 g 81 t
 ORIGIN

Query Match 31.9%; Score 281.2; DB 4; Length 428;
 Best Local Similarity 97.4%; Pred. No. 1.5e-60;
 Matches 339; Conservative 0; Mismatches 3; Indels 6; Gaps 5;

Db 7 gcatggagccctctggagactgggggctcctccctggagatcacccacagagacgagc 66
 |||||||
 Db 87 GCATGGAGCCCTCTGGAGACTGGGGGCTCTCTCTCTGAGATCCACCCCAAGAACGACG 146
 |||||||
 QY 67 tcttgaggtgtgtgtatctacacctctctggagagccctctctacgcccagctctgc 126
 |||||||
 Db 147 TCTTGAGGCTGTGCTGTATCTACCTTCCTGAGAGCCCTCTGAGATCCACCCCAAGAACGACG 206
 |||||||
 QY 127 cgtctcgaag 186
 |||||||
 Db 207 CGTCTCTCCAA-CAGAGAGAGATACC--AGTGGCTTCGAGTGTGCTCCCAAGTGCAGTCAG 263
 |||||||
 QY 187 gttatcgttgaagaag 246
 |||||||
 Db 264 GTTATCGTGTGAAGAGAGCCCTGGCGGAGCTGAGAGGAGACAGTGTGTAACCTGCCCCCTC 323
 |||||||
 QY 247 caggcacctacatgcccacacatgcccacatgcccacatgcccacatgcccacatg 306
 |||||||
 Db 324 CA-GCAGCTACATGCGCCACCTCAATGGCTTAAGCAAGTGTCTGTCAATGTGTG 382
 |||||||
 QY 307 accacacatgagcctgctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 354
 |||||||
 Db 383 ACCAGGCAAT-GGCTTCGGCGCA-CGGAACATGCTCCAGACAGAGA 428

RESULT 7
 AA021617 457 bp mRNA EST 30-JAN-1997
 LOCUS
 DEFINITION z669d02.r1 Soares retina N2b4HR Homo sapiens cDNA clone

IMAGE:364227 5', mRNA sequence.
 AA021617 GI:1485315
 VERSION
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 457)
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chappell, B.,
 Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Harkins
 M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Maritz, E., Moore
 B., Morris, M., Parsons, J., Prange, C., Riklin, L., Rohlfing, T.,
 Schellenberg, K., Soares, M.B., Tan, F., Thierly-Meg, J., Trevas, E.,
 Underwood, K., Woldmann, P., Waterston, R., Wilson, R. and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)

JOURNAL

MEDLINE

COMMENT

Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 1546 Std Error: 0.00
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 364.

FEATURES

Source

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 /db_xref="taxon:9606"
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 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dt) primer [5'
 TGTACCAATCTGAAGTGGAGCGGCGCTTCTCCCTGAGATCCACCCCAAGAACGACG
 15'-TGTACCAATCTGAAGTGGAGCGGCGCTTCTCCCTGAGATCCACCCCAAGAACGACG
 1. Double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pRT3D vector
 (Pharmacia). The retinas were obtained from a 55 year old
 Caucasian and total cellular poly(A)+ RNA was extracted 6
 hrs after their removal. The retina RNA was kindly
 provided by Roderick R. McInnes M.D. Ph.D. from the
 University of Toronto. Library constructed by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT 83 a 145 c 135 g 86 t 8 others
 ORIGIN

Query Match 30.8%; Score 271; DB 1; Length 457;
 Best Local Similarity 94.8%; Pred. No. 5.5e-58;
 Matches 330; Conservative 0; Mismatches 12; Indels 6; Gaps 5;

QY 7 gcatggagccctctggagactgggggctcctccctggagatcacccacagagacgagc 66
 |||||||
 Db 107 GNATGAGCCTCTCTGAGACTGGGGGCTCTCTCTCTGAGATCCACCCCAAGAACGACG 166
 |||||||
 QY 67 tcttgaggtgtgtgtatctacacctctctggagagccctctctacgcccagctctgc 126
 |||||||
 Db 167 TCTTGAGGCTGTGCTGTATCTACCTTCCTGAGAGCCCTCTGAGATCCACCCCAAGAACGACG 226
 |||||||
 QY 127 c-gtctcgaag 183
 |||||||
 Db 227 CAGTCTGCAAGAGAGAGAGATCCAGTGGCTTCGAGTGTGCTCCCAAGTGCAGTCC 286

OY	184	caggcttaccgtgtgaagaag - aggcctctggggggaagctgacgggacacgtgtgtgaacccctgc	242
Db	287	AAGGTTATTCGTGAAGGAAGCCCTGGGGGACCTGCAGGGGACAGTGTGTGAACCTCGC	346
OY	243	cctccagcaccctacatttgcaccactcaatctgacctgaagcaagtctctgcagtctgcgaatg	302
Db	347	CCTCCAGGCACTCAATGATGGCCACCTCAATAGGCGCTAAGCAANTGTCTGCAGTGCACCAATG	406
OY	303	- tctgacccacagccaatgggcctctgcg - gcgaagccgaactctctccagga	348
Db	407	TTTGACACCCACGCACTAGGAGCCTTCGCGCGGACCGGAACTCTCTCCAGGA	454

RESULT	8			
LOCUS	AI356409/c			
DEFINITION	AI356409	823 bp	mRNA	EST
	q22b9.11.x1	NC1:CGAF.CLL1	Homo sapiens cDNA clone IMAGE:2028068	16-FEB-1999
	similar to	TR:Q92956	Q92956	HERPESVIRUS ENTRY MEDIATOR. ; mRNA
ACCESSION	AI356409			
VERSION	AI356409.1			
KEYWORDS	EST.	GI:4108030		
SOURCE	human.			

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 823)
REFERENCE AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/cgap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D.

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Ash Allaladeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
cDNA library preparation: M. Bento Soares, Ph.D.
cDNA library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnsl.gov/db/brp/image/image.html
Insert length: 1470 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 454.

FEATURES	Location/Qualifiers
source	1. .823

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/clone="IMAGE:2028068"
/clone_lib="NCI-CGAP_CLL1"
/tissue_type="B-cell, chronic lymphocytic leukemia"
/lab_host="DH108"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site.1: Not I; Site.2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACATCTCAAGTGGAGGCGCCGCGATGCTTTTATTTTATTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."

```

Query Match	30.3%;	Score 267;	DB 19;	Length 823;
Best Local Similarity	86.8%;	Pred. No. 6.1e-57;		
Matches 328; Conservative	0;	Mismatches 46;	Indels 4;	Gaps 3

Oy 504 cccccgggaccttctctcccaatgtagaccctygaggaatgtcagcaccagaccaaatgac 5633
 ||||| | ||| | |||| | ||||| | ||||| | ||| ||||
 Db 821 cccccccgggctttttccccaatgggacccgaaaggaagtacagaccgacccccagctgc 7622

OY	564	agctgcgcgtgtagaagaagccggagagctcggagcaagagcctccacactggtatggtgtt	623
Db	761	AGCTCGCTGGTGAGACAGGGGCGGAAGCTGG--ACGCAAGCTTNCANATGATATGATGTTT	704
OY	624	ctctcgaaggaacctgcgtcatctgattgtttgtctccacaaattgagccatacatatggtg	683
Db	703	CTTCAAGGGACCTGTCATCTCATTTGTTTGGCTCCACAGTGGGCGCTAAATCATATGTGTG	644
OY	684	aaaagaagaagccaaggggtgtagttagtcaagtgtagtctctcgtlccacgagaaaga	743
Db	643	AAAAGAAGAAGCCAAAGGGGTGATGTAGTCAAGTGAT-CTTCATCATCCAGCGGAAAGA	585
OY	744	caaggaagcagaagtgtagggccaaagtcatttgaagccctcagaagccctccggaagtcacc	803
Db	584	CAGGAGCAGAAAGGTGAGGCCACACGATTTGAGGCCCTCGCAGGCCCTCCGGAGCT-ACC	526
OY	804	acggttgcccgtagggagagacaatacctctaatcagggggagggagccaaacacttgacc	863
Db	525	ACGGTGCCCGTGGAGGAGACATACCTTCATTCACGGGGAGGAGACCCAAACCACTGACCC	466
OY	864	acagactctgaccccca	881
Db	465	ACAGACTCTGCACCCCGA	448

RESULT	9	
LOCUS	BE386504	
DEFINITION	BE386504 482 bp mRNA EST IMAGE:3614650 5'	
ACCESSION	601273747	NIH_MGC_20 Homo sapiens CDNA clone
VERSION	BE386504	mRNA sequence.
KEYWORDS	BE386504.1	GI:931869 EST.

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Homo sapiens					
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:					
Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo:					
1 (bases 1 to 482)					
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/ .					
National Institutes of Health, Mammalian Gene Collection (MGC)					
Unpublished. (1999)					
Contact: Robert Strausberg, Ph.D.					

1 (bases to 482)
NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: ATCC/DCTD/DRP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L10CM277 row: h column: 11
High quality sequence start: 7
High quality sequence stop: 480.

FEATURES	Location/Qualifiers
source	1. .482

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3614650"
/clone_lib="NIG_MGC-20"
/tissue_type="melanotic melanoma"
/lab_host="DH10b (phage-resistant)"
/note="Organ: skin; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into pGEMT4ho1 vector. The following 5'

```

BASE COUNT	69 a	173 c	137 g	103 t
------------	------	-------	-------	-------

ORIGIN

were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

BASE COUNT 53 a 84 c 78 g 36 t

Query Match 26.0%; Score 228.8; DB 7; Length 251;
Best Local Similarity 96.8%; Pred. No. 2,1e-47;
Matches 244; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

OY 256 acattgccacactcaatgagcctaagcagtgctcagtgccaatgtgtgaccagcca 315
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1 ACATTGACACACTCAATGAGCCTAAGCAAGTCTGCACTGCCAATGTGTACCCAGCCA 60
OY 316 tgggcttgagcgagcgagcagcagcagcagcagcagcagcagcagcagcagcagc 375
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 61 TGGGCTGGCGGCGAGCGGAACTGCTCAGAGACAGAAAGCGCGTGTGTGTCAG-C 119
OY 376 cagcgcacttctgcatgctcaggaagcgagcagcagcagcagcagcagcagcagc 435
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 120 CAGGCACTTCTGTCATGCTCAGAGCGGAGCACTGCGCGCGCGCATACGCCA 179
OY 436 cctcagcccgagcagaggtgcagagagagagcagcagagtcagagacccctgtgtc 495
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 180 CCTCCAGCGCGGCGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 239
OY 496 agaactgcccc 507
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 240 AGAAGTGGCCCC 251

RESULT 12
A1479005/c 719 bp mRNA EST 14-APR-1999
LOCUS tm29f10.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2158027 3'
DEFINITION similar to TR:Q92956 Q92956 HERPESVIRUS ENTRY MEDIATOR. ;, mRNA
sequence.
ACCESSION A1479005.1 GI:4372173
VERSION A1479005
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 719)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bhrp/image/image.html
Insert Length: 1356 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 455.
Location/Qualifiers

FEATURES

1. 719
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2158027"
/clone_lib="NCI_CGAP_CLL1"

BASE COUNT 138 a 228 c 211 g 141 t 1 others

Query Match 24.8%; Score 218.6; DB 21; Length 719;
Best Local Similarity 95.2%; Pred. No. 9e-45;
Matches 257; Conservative 0; Mismatches 10; Indels 3; Gaps 3;

OY 612 gatagtgtgtctctcagagagagcctcgtcatcgtcattgttgcacagttgacct 671
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 719 GTATGGGTGTTTCTCTAGGAAAGCTGTGTCATGTCATTTGTTGCTCCAGTTGGCCCTA 660
OY 672 atcatatgttgaaagaagaagcaaggggtgatgtagtcagagtgatcgtcttcgtc 731
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 659 ATCATATGTGTG-AAAGAAAGAAAGCCAAAGGGTGATGTAAGTCAAGTGATC-TCTCCGTC 602
OY 732 cagcgagaaagacagagagagagagagtgagagcagacagtcattttagagcccgagagccct 791
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 601 CAGCGG-AAAGACAGAGGAGGAGAGGTGAGGCGCACTGTGAGGCGGCGGCGGCGGCGG 543
OY 792 ccgagagcaccacagcgagcgagcgagagagacacataccatcagcagagagagccca 851
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 542 CCGGACGTCACACAGCGTGCGCGGTGAGAGACATATACCTCATTCCAGGGAGAGGCCCA 483
OY 852 aaccactgacccaagacactctgaccccca 881
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 482 AACCACTGACCCACAGACTCTGCACCCCGA 453

RESULT 13
AA088363 426 bp mRNA EST 24-OCT-1996
LOCUS 2182C02.r1 StrataGene colon (#937204) Homo sapiens cDNA clone
DEFINITION IMAGE:511106 5', mRNA sequence.
ACCESSION AA088363
VERSION AA088363
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 426)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Treaskis, E.,
Underwood, K., Woldmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
9704478
Contact: Willson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28W13 rev2 from Amersham
High quality sequence stop: 269.
Location/Qualifiers

FEATURES


```

source
1. .426
/organism="Homo sapiens"
/db_xref="GDB:3843601"
/db_xref="taxon:9606"
/clone_lib="Stratagene colon (#937204)"
/tissue_type="tumor"
/lab_host="T84 carcinoma cell line"
/label="SOLR cells (kanamycin resistant)"
/ECORI_Site2: XhoI; Cloned unidirectionally.
/insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor
sequence: 5' GAATTCGACGAG 3' ~3' adaptor sequence: 5'
CTCGAGTTTCTTTTCTTTT 3'

BASE COUNT      94 a      132 c      128 g      70 t      2 others
ORIGIN

Query Match      24.2%; Score 213.6; DB 2; Length 426;
Best Local Similarity 94.3%; Pred. No. 1.5e-43;
Matches 298; Conservative 0; Mismatches 9; Indels 9; Gaps 7;

QY 204 gctcgaggagagctcgagcgacagctgtgtgaacc--tgccctcaggacacattgc 262
|||||
Db 1 GCCTGCGGGAGCTGACGCGGACAGTGTGTGACCCATGCGCTCCAGGACCTACATTGC 60

QY 263 ccacctcaatggccttaagcaagtgtctgcagtgccaaatgtgttaccacacattggagcct 322
|||||
Db 61 CCACCTCAATGGCTTAAGCAAGTGTGTGACCTCCAAATGTGTACCCAGCATGGGCTT 120

QY 323 ggcgcgagcgcgagactgtctccagagagaagaacgcgtgtgtgtgttcagccagagcca 382
|||||
Db 121 GCGGCGGCA-CCGGAATGCTCCAGACAGAACGCCGTGTGTGTGCGTGCAG-CCAGGCGCA 178

QY 383 ctcttcgatcgttcagagacggagacacgtgcgcgtgtgcgcgttaagcaccttca- 441
|||||
Db 179 CTCTGATGCTCCAGACGCGGACCACTGCGCGCTGCGCTTACGCGCACCTCCAA 238

QY 442 -ggccggcgccagaggtgtgc--agaagagagcaccca--gaagtcagacaccc-tgtgtca 496
|||||
Db 239 GCCCGGGGCGAGAGGTGCGAAGAGGAGGCCCGAAGAAATCAGACACCTTGTGTCA 298

QY 497 gaactgccccccgggg 512
|||||
Db 299 GAACCTGCCCGCGGG 314

RESULT 14
BE699740/c 237 bp mRNA EST 12-SEP-2000
LOCUS BE699740
DEFINITION BR699740
ACCESSION BE699740
VERSION BE699740.1 GI:10087482
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 237)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research

```

```

FEATURES
source
1. .237
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN0087"
/dev_stage="Adult"
/note="Organ: nervous,normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
Location/Qualifiers
1. .237

BASE COUNT      32 a      79 c      78 g      48 t
ORIGIN

Query Match      24.0%; Score 211.4; DB 111; Length 237;
Best Local Similarity 98.7%; Pred. No. 4.9e-43;
Matches 234; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 346 ggcagagagacgcgtgtgtgtgttcagccagcgacattctcatcgttcagagaggg 405
|||||
Db 237 GGACAGAGAACGCCGTGTGTGTGCGTGCAGCCAGGCCACTTCTGATCTGCAGAGCGGG 178

QY 406 accactgagcgcgtgtgcgcgttaagccacatcagccggcgagaggtgtcagaag 465
|||||
Db 177 ACCACTGCGCGCGTGTGCGCTTACGCCACTGCACGCCGCGGCGAGAGGTCAGAAAG 118

QY 466 gaggcacggagatcagagacacctgtgtagaactgtccccggggagacttctccca 525
|||||
Db 117 GAGGCACCGAGAGTACAGACACCTGTGTGAGAACTCCCGCGGAGACCTTCTGCCA 58

QY 526 atggaccctggaggaatgtcacacca-gaccaagtgcagctgcgtgtgtgacgaag 581
|||||
Db 57 ATGGGA-CTTGAGAGATGTTCAGCACGACCAAGTGCAGTGGCTGTGTGACGAAG 2

RESULT 15
AM978536/c 682 bp mRNA EST 02-JUN-2000
LOCUS AM978536
DEFINITION EST380645 MAGE resequences, MAGEP Homo sapiens cDNA, mRNA sequence.
ACCESSION AM978536
VERSION AM978536.1 GI:8169803
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 682)
Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org

```


Plate: 394
Seq primer: Forward.

FEATURES
Location/Qualifiers
source 1. .682

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="MAGE resequences, MAGP"
/note="Vector: pBluescriptskm"

BASE COUNT 123 a 219 c 205 g 135 t
ORIGIN

Query Match

Best Local Similarity 24.0%; Score 211; DB 97; Length 682;
Pred. No. 7.3e-43;

Matches 217; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```
OY 655 gctcacagttggcctaataatgltgaaagaagaagccaagggtgtagtca 714
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 682 GCTCCAGTTGCGCTTATATATGTGTAAGAAAGATAGCCAAAGGGTGATGTCA 623

OY 715 agtgcacgtctccgtccagcgcgaagaacagagagcagaagtcgagccacagtcattg 774
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 622 AGGTGATGTCTCTCGTCCAGCGGAAAGACAGAGGCGAAGGTGAGGCCACAGTCATTG 563

OY 775 aggccttcgaagccctccgcgaagtcacacagtcgcccgtgagagagaacaataacctcat 834
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 562 AGGCCCTGTCAGGCCCCCTCCGAACGTCACCCCGGTGCGCGTGAGAGAGACAATACCTCAT 503

OY 835 tcacgggagagagcccaaacacactgacccacagactctgcaccccgga 881
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 502 TCACGGGAGAGGCCCAACACACTGACCCACAGACTTTGCACCCCGA 456
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Search completed: April 24, 2001, 19:23:30
Job time: 7869 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2001, 17:31:39 ; Search time 17.99 Seconds

(without alignments)
899.233 Million cell updates/sec

Title: US-08-741-095b-26

Perfect score: 1578
Sequence: 1 MEPPGDMPPWRSTPRIDV.....VTVAVETIPSTGRSPNH 283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0401.*
1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
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4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT.*
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6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT.*
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18: /SID56/gcgdata/geneseq/geneseq/AA1997.DAT.*
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21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1578	100.0	283	17 W05809	Human tumour necro
2	1578	100.0	283	19 W69238	Herpesvirus entry
3	1578	100.0	283	20 Y06488	Human tumour-asso
4	1578	100.0	283	21 Y94721	Human TR2-receptor
5	1578	100.0	283	21 Y93695	Amino acid sequenc
6	1578	100.0	283	21 Y93348	Human PRO509 anti
7	1575	99.8	283	19 W60045	Human TNF receptor
8	1575	99.8	283	19 W67591	Human tumour necro
9	1575	99.8	283	21 Y94717	Human TR2-receptor
10	1572	99.6	283	20 W95031	Tumour necrosis fa
11	1570	99.5	283	18 W12659	Human herpes simpl

12	1570	99.5	283	20 Y05797	Herpes virus entry
13	1373.5	87.0	277	21 Y79207	Membrane-bound her
14	1068	67.7	193	21 Y79204	Soluble herpesvitu
15	1060	67.2	197	21 Y79205	Soluble herpesvitu
16	1058	67.0	186	21 Y79206	Soluble herpesvitu
17	604.5	38.3	185	19 W60046	Human TNF receptor
18	604.5	38.3	185	21 Y94716	Human TR2-receptor
19	604.5	38.3	240	17 W05810	Human tumour necro
20	393	24.9	136	19 W60047	Human TNF receptor
21	393	24.9	161	21 Y94719	Human TR2-receptor
22	377.5	23.9	134	17 W05811	Human tumour necro
23	332	21.0	278	21 Y95322	Pig costimulatory
24	276.5	17.5	281	21 Y94715	Murine CD40 protei
25	268.5	17.0	277	20 Y32191	CD40 protein. Uni
26	267.5	17.0	276	20 Y33499	Human CD40 protein
27	267.5	17.0	277	14 R38859	CD40 protein. Hom
28	267.5	17.0	277	20 Y52701	Human CD40 protein
29	267.5	17.0	277	22 B50520	Human tumour necro
30	267.5	17.0	277	22 B37807	Human CD40. Homo
31	260	16.5	325	13 R27865	Rabbit fibroma vir
32	260	16.5	325	16 R85071	Shope fibroma viru
33	260	16.5	461	16 R72504	p75 Tumour Necrosi
34	259	16.4	183	16 R77421	BamP delta53 nerv
35	259	16.4	225	21 Y77463	Primate protein se
36	259	16.4	235	19 W59665	Human soluble tumo
37	259	16.4	235	19 W52270	Tumour necrosis fa
38	259	16.4	235	20 W89234	Tumour necrosis in
39	259	16.4	235	21 Y54443	Amino acid sequenc
40	259	16.4	235	21 Y54443	Wild type N-beta
41	259	16.4	235	22 B37685	Human 40 kDa TNF I
42	259	16.4	248	21 Y94718	Human type 2 tumou
43	259	16.4	461	12 R11001	40KD TNF inhibitor
44	259	16.4	461	12 R11141	Human TNF-R deduce
45	259	16.4	461	14 R42058	Fibroblast derived

ALIGNMENTS

RESULT	1
ID	W05809
W05809	standard; Protein; 283 AA.
AC	W05809;
XX	
DT	30-JUN-1997 (first entry)
XX	
DE	Human tumour necrosis factor receptor.
XX	
KW	Human; tumour necrosis factor; TNF; receptor; treatment;
KW	activation; inhibition; identification; agonist; antagonist;
KW	stimulation; T cell; differentiation; mediation; immune;
KW	antiviral; response; regulation; growth; protection; HIV;
KW	radiation; Chlamydia; infection; immunodeficiency; virus;
KW	autoimmune disease; inflammation; septic shock; cerebral; malaria;
KW	cachexia; B cell; cancer; graft; host; reaction; rejection;
KW	prevention; apoptosis; cytotoxicity; hybridisation probe;
KW	detection; antibody; reagent.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	Peptide 1..38
FT	/label= sig_peptide
FT	39..283
FT	/label= mat_peptide
XX	
PN	W09634095-A1.
PD	31-OCT-1996.
XX	
PF	27-APR-1995; 95MO-US05058.
XX	

PR 27-APR-1995; 95MO-US05058.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Gentz R, NJ J, Rosen CA;
XX
DR WPI: 1996-497627/49.
DR N-PSDB: T40048.
XX
PT New nucleic acid encoding a human tumour necrosis factor receptor -
PT useful for treatment of auto-immune diseases etc., in diagnosis and
PT for drug screening
XX
PS Claim 1; Pages 47-48; 73pp; English.
XX
CC The present sequence is the human tumour necrosis factor (TNF)
CC receptor, which may be used for the identification of TNF receptor
CC agonists or antagonists. TNF receptor agonists inhibit tumour
CC growth, stimulate cell (e.g. T cell) differentiation, mediate the
CC immune and antiviral responses, regulate growth, protect against
CC radiation and Chlamydia infection, and can be used to treat
CC immunodeficiencies, e.g. human immunodeficiency virus. Antagonists
CC can be used to treat T cell mediated autoimmune disease.
CC Inflammation, septic shock, cerebral malaria, cachexia or B cell
CC cancers, to inhibit graft-host reactions and to prevent apoptosis
CC or cytotoxicity. Fragments of the TNF receptor encoding DNA can be
CC used as hybridisation probes for detecting related genes.
CC Antibodies against the protein can be used as reagents for
CC detecting/measuring soluble forms of protein in the circulation.
XX
SQ Sequence 283 AA;

Query Match 100.0%; Score 1578; DB 17; Length 283;
Best Local Similarity 100.0%; Pred. No. 3.4e-121;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEBPGDMGPPMRSTPRTDVLRLVLYLFLGAPCYAPALPSCKEDEYPVSECCPKCSFG 60
Db 1 meppgdmgppmrstprtldvlrlvlylflgapyapalpsckedeypvsgccpkcsfg 60

QY 61 YRVKACGELTGTVCCEPCPGPTIYIAHLNGLSKLQCCOMCDPAMGLASRNCSTENAVCG 120
Db 61 yrvkaacgeltgtvccepcpgptiyiahnglskclqccomcdpamglasrncstenaavcg 120

QY 121 CSPGHCTIVODGDHCAACRAATSSPGQRVQKGTESQDTLQNCNCPGTSPNGTLEECQ 180
Db 121 cspghctivodgdhcaacraatsspgqrvykgtesqdtlqncncpgtspngtleecq 180

QY 181 HQTGCSWLTKAGAGTSSSHMMWMLFSLVIVYVCTGGLICVKKRPRGDDVAVIYS 240
Db 181 hqtgcswltkagagtssshmmwmlfslgslvivycstvglllcvkrtprgddvavkviys 240

QY 241 VQRRKQAEAGEATVIALQAPPDVTVAVEETIPSTGRSPNH 283
Db 241 vqrrkqaeageatvialqapdpvtvaveetipstgrspnh 283

RESULT 2
ID W69238 standard; Protein; 283 AA.
XX
AC W69238;
XX
DT 21-OCT-1998 (first entry)
XX
DE Herpesvirus entry mediator protein.
XX
KW Entry mediator gene; herpesvirus; HVEM; tumour necrosis factor receptor;
KW gene expression regulator; cellular stress; inflammatory response;
KW lymphocyte activity regulator; autoimmune response.
XX
OS Homo sapiens.

XX
PN WO9825967-A1.
XX
PD 18-JUN-1998.
XX
PF 05-DEC-1997; 97MO-US22278.
XX
PR 12-DEC-1996; 96US-0032705.
XX
PA (GENE) GENENTECH INC.
XX
PI Ashkenazi AJ, Marsters SA;
XX
DR WPI: 1998-348457/30.
DR N-PSDB: V44852.
XX
PT Herpesvirus entry mediator polypeptide, HVEM - useful, e.g. in
PT assays for HVEM and to produce antibodies and transgenic animals,
PT e.g. for drug screening
XX
PS Claim 1; Fig 1; 46pp; English.
XX
CC This sequence is the herpesvirus entry mediator (HVEM) protein of
CC the invention. The protein is useful in quantitative diagnostic assays
CC for HVEM, in affinity purification of HVEM from recombinant cells/natural
CC sources and in competitive-type receptor binding assays. It can also be
CC used to generate antibodies, also useful in diagnostic assays for HVEM
CC and affinity purification of HVEM. HVEM is believed to be a member of the
CC tumour necrosis factor receptor (TNFR) family, and transient transfection
CC of HVEM into human 293 cells caused marked activation of certain
CC transcription factors, e.g. AP-1, suggesting that HVEM is involved in
CC regulating gene expression in response to infectious stimuli and cellular
CC stress. The predominant expression of HVEM mRNA in lymphocyte-rich
CC tissues (e.g. spleen and peripheral blood) also suggested it may be a
CC receptor in regulating lymphocyte activity. Antibodies produced may be
CC therefore be useful therapeutically, e.g. antagonistic antibodies may be
CC useful to block excessive inflammatory/autoimmune response resulting from
CC e.g. AP-1 induction, whilst agonistic antibodies may enhance HVEM
CC regulation of such induction. The DNA may be used diagnostically, e.g.
CC to determine if DNA and/or RNA encoding HVEM is present in cells, and to
CC prepare HVEM polypeptide recombinantly. It is also useful to produce
CC non-human transgenic animals (e.g. mice or rats), especially knockout
CC animals containing cells with an altered gene encoding HVEM polypeptide.
CC Such animals are useful in the development and screening of
CC therapeutically useful reagents.
XX
SQ Sequence 283 AA;

Query Match 100.0%; Score 1578; DB 19; Length 283;
Best Local Similarity 100.0%; Pred. No. 3.4e-121;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEBPGDMGPPMRSTPRTDVLRLVLYLFLGAPCYAPALPSCKEDEYPVSECCPKCSFG 60
Db 1 meppgdmgppmrstprtldvlrlvlylflgapyapalpsckedeypvsgccpkcsfg 60

QY 61 YRVKACGELTGTVCCEPCPGPTIYIAHLNGLSKLQCCOMCDPAMGLASRNCSTENAVCG 120
Db 61 yrvkaacgeltgtvccepcpgptiyiahnglskclqccomcdpamglasrncstenaavcg 120

QY 121 CSPGHCTIVODGDHCAACRAATSSPGQRVQKGTESQDTLQNCNCPGTSPNGTLEECQ 180
Db 121 cspghctivodgdhcaacraatsspgqrvykgtesqdtlqncncpgtspngtleecq 180

QY 181 HQTGCSWLTKAGAGTSSSHMMWMLFSLVIVYVCTGGLICVKKRPRGDDVAVIYS 240
Db 181 hqtgcswltkagagtssshmmwmlfslgslvivycstvglllcvkrtprgddvavkviys 240

QY 241 VQRRKQAEAGEATVIALQAPPDVTVAVEETIPSTGRSPNH 283
Db 241 vqrrkqaeageatvialqapdpvtvaveetipstgrspnh 283

```

RESULT 3
ID Y06488 standard; Protein; 283 AA.
XX
AC Y06488;
XX
DT 27-SEP-1999 (first entry)
XX
DE Human tumour-associated protein PRO509.
XX
KW PRO1112; UNQ555; cancer; tumour necrosis factor receptor;
KM diagnosis; therapy; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 201..225
FT /note= "transmembrane domain"
FT Domain 226..283
FT /note= "cytoplasmic domain"
XX
PN MO9935170-A2.
XX
PD 15-JUL-1999.
XX
PE 05-JAN-1999; 99MO-US00106.
XX
PR 20-NOV-1998; 98US-0109304.
PR 05-JAN-1998; 98US-0070440.
PR 29-APR-1998; 98US-0083500.
PR 22-MAY-1998; 98US-0086414.
PR 10-JUN-1998; 98US-0088742.
PR 10-NOV-1998; 98US-0107783.
XX
XX (GETH ) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
PI Roy MA, Wood WI;
XX
DR WPI: 1999-430385/36.
DR N-PSDB: X87265.
XX
PT Antibody against proteins expressed in neoplastic cells, useful for
PT tumor diagnosis and treatment
XX
PS Example 1; Fig 24; 162pp; English.
XX
CC This sequence represents human PRO509 (UNQ329), a protein encoded
CC by the novel cDNA clone DNA50148 (see X87264), and a member of the
CC tumour necrosis factor receptor family. Amplification of DNA50148
CC was observed in various tumour tissues, suggesting a role in tumour
CC formation or growth. Antagonists (e.g. antibodies) directed to
CC PRO509 may have use in cancer therapy. The invention identifies
CC 14 genes (see X87254-67) that are amplified in the genome of tumour
CC cells. Such amplification is expected to be associated with
CC overexpression of the gene product and to contribute to tumorigenesis.
CC The encoded proteins (see Y06477-90) may be useful targets for the
CC diagnosis and/or treatment (including prevention) of certain cancers,
CC and may act as predictors of the prognosis of tumour treatment.
CC Antibodies that bind the proteins are claimed and used in claimed
CC cancer diagnostic kits.
XX
SO Sequence 283 AA;

```

```

Query Match 100.0%; Score 1578; DB 20; Length 283;
Best Local Similarity 100.0%; Pred. No. 3,4e-121;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 MPPGDMDGPPPPRSPPRDVLRVLYLTFGLGAPCYAPALPSCSKDEVPVSGCCPKKSPG 60
DB 1 MPPGDMDGPPPPRSPPRDVLRVLYLTFGLGAPCYAPALPSCSKDEVPVSGCCPKKSPG 60

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```

OY 61 YRVKACGELTGTVCERPPEPTVIAHLNGLSKCLQGCWCDPAMGLRARNCRTEANVCG 120
DB 61 YRVKACGELTGTVCERPPEPTVIAHLNGLSKCLQGCWCDPAMGLRARNCRTEANVCG 120
OY 121 CSPGHFCLVQDGDHCAACRAVATSSPGORVOKGTEBODTLQCNCPPTGSPNLTLECCQ 180
DB 121 CSPGHFCLVQDGDHCAACRAVATSSPGORVOKGTEBODTLQCNCPPTGSPNLTLECCQ 180
OY 181 HQTGCSMLVTKAGAGTSSSHVWMPFLSGSLVTVICSTVGLITCVKRRKPRGDVVKYIVS 240
DB 181 HQTGCSMLVTKAGAGTSSSHVWMPFLSGSLVTVICSTVGLITCVKRRKPRGDVVKYIVS 240
OY 241 VQRRKROEAGEATVIEALQAPPDVTVAVERTPSPFTGRSPNH 283
DB 241 VQRRKROEAGEATVIEALQAPPDVTVAVERTPSPFTGRSPNH 283

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```

RESULT 4
ID Y94721 standard; Protein; 283 AA.
XX
AC Y94721;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human TR2-receptor protein sequence.
XX
KW Tumour necrosis factor-receptor related protein; TR2; human; cancer;
KW chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease;
KW immunodeficiency; metastasis; hemolytic anaemia; asthma; X-linked SCID;
KW severely combined immunodeficiency; apoptosis inhibition;
KW Alzheimer's disease; Parkinson's disease; Crohn's disease.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..38
FT /note= "Signal peptide"
FT Protein 39..283
FT /label= "TR2 receptor"
XX
PN WO200056405-A2.
XX
PD 28-SEP-2000.
XX
PE 22-MAR-2000; 2000MO-US07521.
XX
PR 22-MAR-1999; 99US-0125683.
PR 26-MAR-1999; 99US-0126522.
PR 20-MAY-1999; 99US-0135169.
PR 06-AUG-1999; 99US-0147383.
XX
XX (NIJ/) NI J.
XX PA (ROSE/) ROSEN C A.
XX PA (GENTZ/) GENTZ R L.
XX
PI NI J, Rosen CA, Gentz RL;
XX
DR WPI: 2000-594519/56.
DR N-PSDB: A28149.
XX
PT Nucleic acid molecule encoding a human tumor necrosis factor receptor 2
PT and its two splice variants, useful for treating arthritis or
PT inflammation, cancer (such as follicular lymphomas) and
PT immunodeficiency disorders -
XX
PS Disclosure; Page 370; 373pp; English.
XX
CC This invention relates to an isolated nucleic acid molecule encoding a
CC human tumour necrosis factor(TNF)-receptor related protein TR2. Included
CC in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.
CC The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a

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CC member of the TNFR superfamily. The invention includes a method for the
 CC treatment of arthritis or inflammation using an antibody directed against
 CC a fragment of the TR2 protein. TR2 its agonists, antagonists and
 CC antibodies exhibit cytostatic, dermatological, antianemic,
 CC immunosuppressive, antiallergic, antiarthritic, antiasthmatic,
 CC antiinflammatory, neuroprotective, nootropic, antiparkinsonian, and
 CC cerebroprotective activity. The methods are useful for treating arthritis
 CC or inflammation, cancer (such as follicular lymphomas, carcinoma with p53
 CC mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an
 CC immunodeficiency or for enhancing an in vivo leukocyte response to an
 CC antigen. Anti-TR2 antibodies are useful for treating, inhibiting or
 CC preventing autoimmune diseases (such as autoimmune hemolytic anaemia,
 CC dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and
 CC inflammatory myopathies) and immunodeficiency disorders (such as severely
 CC combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative
 CC disorder, or Nezelof syndrome-combined immunodeficiency with Igs). TR2,
 CC TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or
 CC antagonists are useful for treating or preventing autoimmune diseases and
 CC inhibit the growth, progression and/or metastasis of cancers. They are
 CC also used to activate, differentiate or proliferate cancerous cells or
 CC tissues, and can be used to treat diseases associated with increased cell
 CC survival, or the inhibition of apoptosis, e.g. Alzheimer's disease,
 CC Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful
 CC as sources for generating antibodies, as molecular weight markers.
 CC This sequence represents the TR2 receptor protein of the invention.

XX Sequence 283 AA:

Query Match 100.0%; Score 1578; DB 21; Length 283;
 Best Local Similarity 100.0%; Pred. No. 3.4e-121;

Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPWRSTPRDVLRLVLYLTFGLGAPCYAPALPSCKEDKDEYVSGCCPKCSPG 60
 Db 1 meppgdwppwrstprtdvlrlvlylftlgapcyapalpsckedeyvsgccpcspg 60
 QY 61 YRVKACGELGTGCEPCPGTGYIAHLNGLSKLQCCQCMCDPAMGLRASRNCSTENAVCG 120
 Db 61 yrvkaacgelgtgcepcpgptgyiahlnnglskclqccqcmcdpamglrasrncstrenavcg 120
 QY 121 CSPGHFCTIVODGDHCAACRAVATSSPGRVGKGSTESODTLQNCPCGTFSPNCTLEBCQ 180
 Db 121 cspghfctivodgdhcaacraavatsspgrvkgstesodtlqncpcgtfspnctleecq 180
 QY 181 HQTCGSMVTYTAGAGTSSHHWMMFLSGSLVIVYVCSVGLICVKKRKPNGDVVKYIVS 240
 Db 181 hqtcgsmvttagagtsshhwmmflsgslvivvcsvglilcvkkrrkprgdvkvkivs 240
 QY 241 VQRKQAEAGATVIALQAPPDVTVAVEETIRSFTRGRSPNH 283
 Db 241 vqrkqaeagatvialqappdvtvaveetirsftrgrspnh 283

RESULT 5
 Y93695 ID Y93695 standard; Protein: 283 AA.
 XX Y93695;
 AC Y93695;
 XX 03-OCT-2000 (first entry)
 DT
 XX Amino acid sequence of novel polypeptide PRO509.
 DE
 XX PRO201; PRO292; PRO327; PRO1265; PRO344; PRO347; PRO357;
 KW PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell;
 KW tumorigenesis; cancer; neoplastic cell growth; cell proliferation.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH 1..36
 FT Peptide
 FT /note="signal sequence"

FT Modified-site 81..87
 FT /note="N-myristoylation site"
 FT Modified-site 89..95
 FT /note="N-myristoylation site"
 FT Modified-site 104..110
 FT /note="N-myristoylation site"
 FT Modified-site 110..114
 FT /note="N-glycosylation site"
 FT Modified-site 120..126
 FT /note="N-myristoylation site"
 FT Modified-site 153..159
 FT /note="N-myristoylation site"
 FT Modified-site 173..177
 FT /note="N-myristoylation site"
 FT Modified-site 193..199
 FT /note="N-glycosylation site"
 FT Modified-site 195..201
 FT /note="N-myristoylation site"
 FT Domain 203..222
 FT /note="transmembrane domain"
 FT Modified-site 220..226
 FT /note="N-myristoylation site"
 FT Region 231..234
 FT /note="cell attachment sequence"

WC0200037640-A2.

XX 29-JUN-2000.
 PD 16-DEC-1999; 99WO-US30095.
 PF 22-DEC-1998; 98US-0113296.
 PR 08-MAR-1999; 99WO-US05028.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 15-SEP-1999; 99WO-US21090.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28565.

XX (GETH) GENENTECH INC.

XX Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;
 PI Wood WI;

XX WPI; 2000-452188/39.

XX N-PSDB; A46931.

XX New anti-polypeptide antibody useful in the treatment and diagnosis of
 PT neoplastic cell growth and proliferation -

XX Claim 61; Fig 24; 220pp; English.

XX The present sequence represents a novel human polypeptide. The
 CC specification describes novel polypeptides designated PRO201, PRO292,
 CC PRO327, PRO1265, PRO344, PRO343, PRO347, PRO357, PRO1017,
 CC PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in
 CC the genome of tumour cells. The polypeptides are believed to contribute
 CC to tumorigenesis. The polypeptides are useful target for the
 CC identification of certain cancers, and may act as predictors of the
 CC prognosis of tumour treatment. Antibodies against these polypeptides
 CC are useful in the treatment and diagnosis of neoplastic cell growth
 CC and proliferation in mammals.

XX Sequence 283 AA:

Query Match 100.0%; Score 1578; DB 21; Length 283;

Best Local Similarity 100.0%; Pred. No. 3.4e-121;

Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPWRSTPRDVLRLVLYLTFGLGAPCYAPALPSCKEDKDEYVSGCCPKCSPG 60

```

Db      1 meppgdwpppwrstprtdivrlvlyltflgapcyapalpsckedeyvvgsecpcpkcspg 60
OY      61 YRVEACGELGTGWCPCPGTYIAHNLGSLKCLQCCOMCPAMGLRASRNCSTRTENAVCG 120
Db      61 yrvkeacgelgtvcepcppgtyiahnlglskclqccmcpamglrasncstrenavcg 120
OY      121 CSPGHFCIVDGDHCAACRAVATSSPGQVOKGGETESQDTLCONCPGCTFSPNGLTEECQ 180
Db      121 cspghfcivdgdhcaacraayatspgqvkggtesqdtlcqncppgtfsgnltleecq 180
OY      181 HOTKCSMLVTRKAGAGTSSSHWVWFLSGSLYIVVCTVGLITCVKRRKRGDVKVIVS 240
Db      181 hgtkcsmlvtrkagagtssshvwwflsgslviviavcstvglllcvkrrkprgdvkvivs 240
OY      241 VORRKEAGEATVIEALQAPPDVTVAVEETIPSTFGSRPNH 283
Db      241 vqrrkeageatviealqapppdvtvaeeetlpsfgsrpnh 283

RESULT 6
ID      Y95348
XX      Y95348 standard; Protein; 283 AA.
AC      Y95348;
DE      25-SEP-2000 (first entry)
XX      Human PRO509 antitumour protein.
KW      PRO509; human; antitumour; tumour; therapy; cytostatic;
KW      breast cancer; ovarian cancer; renal cancer; colorectal cancer;
KW      uterine cancer; prostate cancer; lung cancer; bladder cancer;
KW      central nervous system cancer; melanoma; leukaemia; neoplasm.
XX      OS Homo sapiens.
XX      FH Key
FH      Peptide
FT      1..36
FT      /label= Signal_peptide
FT      37..283
FT      /label= PRO509
FT      Domain
FT      205..221
FT      /note= "transmembrane domain"
FT      Modified-site
FT      81..87
FT      /note= "N-myristoylation"
FT      Modified-site
FT      89..95
FT      /note= "N-myristoylation"
FT      Modified-site
FT      104..110
FT      /note= "N-myristoylation"
FT      Modified-site
FT      120..126
FT      /note= "N-myristoylation"
FT      Modified-site
FT      153..159
FT      /note= "N-myristoylation"
FT      Modified-site
FT      193..199
FT      /note= "N-myristoylation"
FT      Modified-site
FT      192..201
FT      /note= "N-myristoylation"
FT      Modified-site
FT      220..226
FT      /note= "N-myristoylation"
FT      Modified-site
FT      110..114
FT      /note= "N-myristoylation"
FT      Modified-site
FT      173..177
FT      /note= "Asn is N-glycosylated"
FT      Modified-site
FT      231..234
FT      /note= "Asn is N-glycosylated"
FT      Region
FT      /note= "cell attachment sequence"
XX      MO200037638-A2.
XX      PN
XX      XX 29-JUN-2000.
XX      PD
XX      PF 02-DEC-1999; 99MO-US28565.
XX      XX

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PR      22-DEC-1998; 98US-0113296.
PR      08-MAR-1999; 99MO-US05028.
PR      21-APR-1999; 99US-0130232.
PR      28-APR-1999; 99US-0131445.
PR      14-MAY-1999; 99US-0134287.
PR      20-JUL-1999; 99US-0144758.
PR      26-JUL-1999; 99US-0145698.
PR      15-SEP-1999; 99MO-US21090.
PR      15-SEP-1999; 99MO-US21547.
XX      XX
PA      (GETH ) GENENTECH INC.
XX      XX
PI      Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Marsters SA;
PI      Napier MA, Pitti RM, Wood WI;
XX      XX
DR      WPI: 2000-442668/38.
DR      N-PSDB; A49727.
XX      XX
PT      Novel composition to inhibit neoplastic cell growth or for treating
PT      tumor in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO219,
PT      PRO221, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509 or
PT      PRO866
XX      XX
PS      Claim 19; Fig 24; 172pp; English.
XX      XX
CC      The present sequence is that of human antitumour protein PRO509,
CC      as deduced from a retinal cDNA clone (see A49727). PRO509 shows
CC      homology to members of the human tumour necrosis factor receptor
CC      family such as the lymphotoxin-beta receptor (11 identities) and
CC      CD40 (12 identities). A claimed method for inhibiting the growth
CC      of a tumour cell comprises exposing the tumor cell to PRO179,
CC      PRO207, PRO320, PRO219, PRO221, PRO224, PRO328, PRO301, PRO526,
CC      PRO362, PRO356, PRO509 or PRO866 (see Y95337-49), their agonists or
CC      chimeric polypeptides incorporating them. The tumour is especially
CC      a cancer selected from breast, ovarian, renal, colorectal, uterine,
CC      prostate, lung, bladder and central nervous system cancer, melanoma
CC      and leukaemia. Methods for the recombinant expression of the
CC      antitumour proteins are also provided.
XX      XX
SQ      Sequence 283 AA:

Query Match 100.0%; Score 1578; DB 21; Length 283;
Best Local Similarity 100.0%; Pred. No. 3,4e-121;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 MEPPGDMGPPPMRSTPRTDIVRLVLYLTFLGAPCYAPALPSCKEDEVVGSSECCPKKSPG 60
Db      1 meppgdwpppwrstprtdivrlvlyltflgapcyapalpsckedeyvvgsecpcpkcspg 60
OY      61 YRVEACGELGTGWCPCPGTYIAHNLGSLKCLQCCOMCPAMGLRASRNCSTRTENAVCG 120
Db      61 yrvkeacgelgtvcepcppgtyiahnlglskclqccmcpamglrasncstrenavcg 120
OY      121 CSPGHFCIVDGDHCAACRAVATSSPGQVOKGGETESQDTLCONCPGCTFSPNGLTEECQ 180
Db      121 cspghfcivdgdhcaacraayatspgqvkggtesqdtlcqncppgtfsgnltleecq 180
OY      181 HOTKCSMLVTRKAGAGTSSSHWVWFLSGSLYIVVCTVGLITCVKRRKRGDVKVIVS 240
Db      181 hgtkcsmlvtrkagagtssshvwwflsgslviviavcstvglllcvkrrkprgdvkvivs 240
OY      241 VORRKEAGEATVIEALQAPPDVTVAVEETIPSTFGSRPNH 283
Db      241 vqrrkeageatviealqapppdvtvaeeetlpsfgsrpnh 283

RESULT 7
ID      M60045
XX      M60045 standard; Protein; 283 AA.
XX      AC
XX      M60045;
XX      XX

```

DT 25-SEP-1998 (first entry)
 XX Human TNF receptor related (TR2) protein.
 DE Human: tumour necrosis factor; TNF; herpes simplex virus;
 XX aberrant cell survival; radiation therapy; lymphocyte proliferation;
 KW immune deficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH Peptide
 FT Location/Qualifiers
 FT 1..36
 FT /note= "Signal peptide"
 FT Peptide
 FT 37..283
 FT /note= "Mature peptide"
 FT Domain
 FT 37..200
 FT /note= "Extracellular domain"
 FT Modified-site
 FT 110
 FT /note= "Asparagine-linked glycosylation site"
 FT Modified-site
 FT 173
 FT /note= "Asparagine-linked glycosylation site"
 FT Domain
 FT 201..225
 FT /note= "Transmembrane domain"
 FT 226..283
 FT /note= "Intracellular domain"
 FT Domain
 PN WO9818824-A1.
 XX 07-MAY-1998.
 XX
 XX 30-OCT-1996; 96WO-US18540.
 XX
 XX 30-OCT-1996; 96WO-US18540.
 XX
 XX 30-OCT-1996; 96WO-US18540.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Gentz RL, Hurler MR, Lyn SDP, Ni J, Rosen CA;
 XX
 DR WPI: 1998-272139/24.
 DR N-PSDB: V34509.
 XX
 PT Nucleic acid encoding TR2 tumour necrosis factor family receptor -
 PT and its splice variants, useful for diagnosis and treatment of
 PT diseases involving abnormal cell survival or death, e.g. herpes
 PT simplex infection
 XX
 PS Claim 1; Fig 1; 151pp; English.
 XX
 CC The human tumour necrosis factor (TNF) receptor related protein (TR2) is
 CC a member of the TNF family and displays considerable homology to murine
 CC CD40. It can be used in soluble forms to treat herpes simplex virus
 CC infection and TR2 proteins (or their agonists or antagonists) are used to
 CC treat disease associated with aberrant cell survival. Agonists may also
 CC be used to protect against the effects of radiation therapy and to
 CC stimulate lymphocyte proliferation and differentiation in patients
 CC infected by human immune deficiency syndrome.
 CC
 XX
 SQ Sequence 283 AA;
 XX
 Query Match 99.8%; Score 1575; DB 19; Length 283;
 Best Local Similarity 99.6%; Pred. No. 5.9e-121;
 Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 XX
 OY 1 MEPPGDMGPPPMWSTPRTDVLRLVLTLFLGAPCYAPALPSCKEDEXPVGSECCPKCSPG 60
 DB 1 meppgdmgpppmwstprrtdvlrlvltlflgapcyapalpsckedexpyvgseccpkcspg 60
 OY 61 YRVKACGELTGTCCECPGCTYAHUNGSKICQCMCPAMKLRASRNCSPRENACVCG 120
 DB 61 yrvkacgeltgtccecpgctyahungskicqcmcpamklrarsncsprenavcg 120
 OY 61 yrvkacgeltgtccecpgctyahungskicqcmcpamklrarsncstrenavcg 120
 DB 61 yrvkacgeltgtccecpgctyahungskicqcmcpamklrarsncstrenavcg 120

OY 121 CSPGHECTIVODGHCACRAVATSSPGQRYOKGTESDTLACNCPGTFSPNGTLEEQ 180
 DB 121 cspghectivodghcacravatsspgqryokgtesdltacncpghtfsgpntleeq 180
 OY 181 HQTKCSWLTVKAGAGTSSSHWMMFLSGSLVIVYVSTVGLIICVKKRRKRGVAVYIS 240
 DB 181 hqtkcswlvtkagagtssshwmmflsgslvivyvstvgliicvkkrrkrgvavkivs 240
 OY 241 VOKRROEAGEATVTEALQAPPDVTVAVEETI PSEFGSRSPNH 283
 DB 241 vqkrroageatvtealqapdvttvaveetlpsftgtrspnh 283
 XX
 RESULT 8
 ID W87591
 AC W87591; standard: Protein; 283 AA.
 XX
 AC W87591;
 XX
 DT 17-MAR-1999 (first entry)
 XX
 DE Human tumour necrosis factor receptor-like 2 protein.
 XX
 XX Tumour necrosis factor receptor-like 2; TR2; TNF; human; psoriasis;
 KW systemic lupus erythematosus; idiopathic thrombocytopenic purpura;
 KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
 KW insulin-dependent diabetes mellitus; allergic disorder; cancer; therapy;
 KW atherosclerosis; viral infection.
 XX
 OS Homo sapiens.
 XX
 XX WO9851346-A1.
 XX
 XX 19-NOV-1998.
 XX
 XX 12-MAY-1998; 98WO-US09744.
 XX
 XX 12-MAY-1997; 97US-0046249.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Harrop JA, Holmes SD, Reddy MP, Truneh A;
 XX
 DR WPI: 1999-059689/05.
 DR N-PSDB: V83763.
 XX
 PT Method of treating pathological condition - comprises administering
 PT tumour necrosis factor-2 antibody to patient
 XX
 PS Disclosure; Page 27-28; 35pp; English.
 XX
 CC This sequence represents the human tumour necrosis factor (TNF)
 CC receptor-like 2 (TR2) protein. Antibodies that target the TR2 protein can
 CC be used in the method of the invention to treat pathological conditions.
 CC The method is used to treat systemic lupus erythematosus, idiopathic
 CC thrombocytopenic purpura, rheumatoid arthritis, multiple sclerosis,
 CC psoriasis, inflammatory bowel disease, insulin-dependent diabetes
 CC mellitus, allergic disorders, e.g. asthma, allergic rhinitis and atopic
 CC dermatitis, cancer, e.g. lymphomas and leukemias, atherosclerosis and
 CC viral infections, e.g. Herpes simplex virus and AIDS. The TR2 antibody
 CC is also used to monitor and diagnose abnormalities in TR-2 function,
 CC production or metabolism.
 CC
 XX
 SQ Sequence 283 AA;
 XX
 Query Match 99.8%; Score 1575; DB 20; Length 283;
 Best Local Similarity 99.6%; Pred. No. 5.9e-121;
 Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 XX
 OY 1 MEPPGDMGPPPMWSTPRTDVLRLVLTLFLGAPCYAPALPSCKEDEXPVGSECCPKCSPG 60
 DB 1 meppgdmgpppmwstprrtdvlrlvltlflgapcyapalpsckedexpyvgseccpkcspg 60


```
Db      1 meppgdwppwrrstlptkdvllrlvlyltflgapyapalpsckedeypvsgccpkcspg 60
Oy      61 YRVKACGELTGVCEPCPGTYIAHLNGLSKLCQCCMCDPAMGLRSLRNCSTENAVCG 120
        |||
Db      61 yrvkaacgelgtvcepcpgtyiahnnglskclqccmcpamglrasncstlenavcg 120
Oy      121 CSPGHFCIVDGDHCAACRAVATSSPGQRYOKGTESDTLQNCPCPTGSPNGTLEECQ 180
        |||
Db      121 cspghfcivdgdhcaacrayatsspgqrvkgtesqdtlcqncppgtfapngtleecq 180
Oy      181 HQTCSWLVTKAGAGTSSSHWMMFLSGSLVIVYVCSVGLIICVRRKRGDVVKVIVS 240
        |||
Db      181 hqtcswlvtkagagtssshwmmflsgslvlyvcsvlglllcvkrrkprgdvvkviys 240
Oy      241 VQRKROAEAGATVTEALQAPPDVTYVAEETIPSTGSRPNH 283
        |||
Db      241 vqrkrgeageatvtealqapdpvtvaveetipstfgsrpnh 283

RESULT  9
Y94717  Y94717 standard; Protein; 283 AA.
XX
AC      Y94717;
XX
DT      29-JAN-2001 (first entry)
XX
DE      Human TR2-receptor protein sequence.
XX
KW      Tumour necrosis factor-receptor related protein; TR2; human; cancer;
KW      Chromosome p16.2-p16.3; arthritis; inflammation; autoimmune disease;
KW      Immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID;
KW      severely combined immunodeficiency; apoptosis inhibition;
KW      Alzheimer's disease; Parkinson's disease; Crohn's disease.
XX
OS      Homo sapiens.
XX
FH      Key
FH      Peptide
FT      1..36
        /note="Signal peptide"
FT      37..283
        /label="TR2 receptor"
FT      37..200
        /note="Extracellular domain"
FT      201..225
        /note="Transmembrane domain"
FT      226..283
        /note="Intracellular domain"
FT      Domain
FT      Domain
XX
XX      WO200056405-A2.
XX
XX      28-SEP-2000.
XX
XX      22-MAR-2000; 2000WO-US07521.
XX
XX      22-MAR-1999; 99US-0125683.
XX      26-MAR-1999; 99US-0126522.
XX      20-MAY-1999; 99US-0135169.
XX      06-AUG-1999; 99US-0147383.
XX
XX      (NIJ/) NI J.
XX      (ROSE/) ROSEN C A.
XX      (GENTZ/) GENTZ R L.
XX
XX      NI J, Rosen CA, Gentz RL;
XX
XX      WPI; 2000-594519/56.
XX      N-PSDB; A28135.
XX
PT      Nucleic acid molecule encoding a human tumor necrosis factor receptor 2
PT      and its two splice variants, useful for treating arthritis or
PT      inflammation, cancer (such as follicular lymphomas) and
PT      immunodeficiency disorders -
```

```
XX      Claim 1; Fig 1; 373pp; English.
PS
XX      This invention relates to an isolated nucleic acid molecule encoding a
CC      human tumor necrosis factor (TNF)-receptor related protein TR2. Included
CC      in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.
CC      The TR2 gene is located on chromosome 1 at position p16.2-p16.3. TR2 is a
CC      member of the TNFR superfamily. The invention includes a method for the
CC      treatment of arthritis or inflammation using an antibody directed against
CC      a fragment of the TR2 protein. TR2 its agonists, antagonists and
CC      antibodies exhibit cytostatic, dermatological, antianemic,
CC      immunosuppressive, anti-allergic, antiarthritic, antiasthmatic,
CC      anti-inflammatory, neuroprotective, nootropic, antiparkinsonian, and
CC      cerebroprotective activity. The methods are useful for treating arthritis
CC      or inflammation, cancer (such as follicular lymphomas, carcinoma with p53
CC      mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an
CC      immunodeficiency or for enhancing an in vivo leukocyte response to an
CC      antigen. Anti-TR2 antibodies are useful for treating, inhibiting or
CC      preventing autoimmune diseases (such as autoimmune haemolytic anaemia,
CC      dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and
CC      inflammatory myopathies) and immunodeficiency disorders (such as severely
CC      combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative
CC      disorder, or Nezelof syndrome-combined immunodeficiency with Ig9). TR2,
CC      TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or
CC      antagonists are useful for treating or preventing autoimmune diseases and
CC      inhibit the growth, progression and/or metastasis of cancers. They are
CC      also used to activate, differentiate or proliferate cancerous cells or
CC      tissues, and can be used to treat diseases associated with increased cell
CC      survival, or the inhibition of apoptosis, e.g. Alzheimer's disease,
CC      Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful
CC      as sources for generating antibodies, as molecular weight markers.
CC      This sequence represents the TR2 receptor protein of the invention.
XX
SQ      Sequence 283 AA:
```

```
Query Match          99.8%; Score 1575; DB 21; Length 283;
Best Local Similarity 99.6%; Pred. No. 5,9e-121;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      1 MEPPGDMGPPWRRSTPRTDVLRLVLYITFLGAPCYAPALPSCKEDEVVSGCCPKCSPG 60
        |||
Db      1 meppgdwppwrrstlptkdvllrlvlyltflgapyapalpsckedeypvsgccpkcspg 60
Oy      61 YRVKACGELTGVCEPCPGTYIAHLNGLSKLCQCCMCDPAMGLRSLRNCSTENAVCG 120
        |||
Db      61 yrvkaacgelgtvcepcpgtyiahnnglskclqccmcpamglrasncstlenavcg 120
Oy      121 CSPGHFCIVDGDHCAACRAVATSSPGQRYOKGTESDTLQNCPCPTGSPNGTLEECQ 180
        |||
Db      121 cspghfcivdgdhcaacrayatsspgqrvkgtesqdtlcqncppgtfapngtleecq 180
Oy      181 HQTCSWLVTKAGAGTSSSHWMMFLSGSLVIVYVCSVGLIICVRRKRGDVVKVIVS 240
        |||
Db      181 hqtcswlvtkagagtssshwmmflsgslvlyvcsvlglllcvkrrkprgdvvkviys 240
Oy      241 VQRKROAEAGATVTEALQAPPDVTYVAEETIPSTGSRPNH 283
        |||
Db      241 vqrkrgeageatvtealqapdpvtvaveetipstfgsrpnh 283

RESULT  10
W95031  W95031 standard; Protein; 283 AA.
XX
AC      W95031;
XX
DT      13-MAY-1999 (first entry)
XX
DE      Tumour necrosis factor receptor (TNF-R) related polypeptide TR2.
XX
XX      Tumour necrosis factor receptor; TNF-R; TR1; TR2; TR3; TR4; arthritis;
KW      inflammation; septicemia; autoimmune disease; transplant rejection;
```

KM graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS;
 KM acute respiratory disease syndrome; restenosis, bone disease; cancer;
 KM atherosclerosis; Alzheimer's disease.

XX Unidentified.

XX EP897114-A2.

XX 17-FEB-1999.

XX 04-JUN-1998; 98EP-0304424.

XX 29-AUG-1997; 97US-0057550.

XX 13-AUG-1997; 97US-0055513.

XX 26-AUG-1997; 97US-0056980.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Brigham-burke MR, Young PR;

XX WPI; 1999-134308/12.

PT Identifying agonists and antagonists to tumour necrosis factor
 receptor (TNF-R) related polypeptides (TR1, TR2, TL2 and TL4) -
 useful for treating stroke, Alzheimer's disease and AIDS

PS Disclosure; Page 13-14; 18pp; English.

XX The invention relates to identifying agonists or antagonists to tumour
 CC necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2
 CC and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a
 CC candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2
 CC or TL4 with a candidate compound in the presence of TR1 or TR2; and (b)
 CC assessing the ability of the candidate compound to compete with TR1 or
 CC TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful
 CC for treating diseases caused by imbalance of TL or TR polypeptide levels,
 CC which cause: chronic and acute inflammation, arthritis, septicemia,
 CC autoimmune diseases, transplant rejection, graft vs. host disease,
 CC infection, stroke, ischemia, acute respiratory disease syndrome,
 CC restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis
 CC and Alzheimer's disease. The present sequence represents a TNF-R related
 CC polypeptide TR2.

XX Sequence 283 AA;

Query Match 99.6%; Score 1572; DB 20; Length 283;

Best Local Similarity 99.6%; Pred. No. 1e-120; Indels 0; Gaps 0;

Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPPMWRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDEYVGSCECPKCSPG 60
 DB 1 MEPPGDMGPPPMWRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDEYVGSCECPKCSPG 60
 QY 61 YRKVEACGELTGYCEPCPGPTTYAHLNGLSKLCQCMCPAMGLRARNCSRTENAVCG 120
 DB 61 YRKVEACGELTGYCEPCPGPTTYAHLNGLSKLCQCMCPAMGLRARNCSRTENAVCG 120
 QY 121 CSPGHFICIVDDGDHICACRAVATSSPGORVKGSTESODPLCQCMCPGCTSPNGCTLEECQ 180
 DB 121 CSPGHFICIVDDGDHICACRAVATSSPGORVKGSTESODPLCQCMCPGCTSPNGCTLEECQ 180
 QY 181 HQTGCSMLVTRKAGAGTSSSHMMWMLFSGSLVIVCSTVGLICVKKRRKRGDVVKVIVS 240
 DB 181 HQTGCSMLVTRKAGAGTSSSHMMWMLFSGSLVIVCSTVGLICVKKRRKRGDVVKVIVS 240
 QY 241 VQRRQAEAGEATVIALQAPDVTVAVEETIPSTGRSPNH 283
 DB 241 VQRRQAEAGEATVIALQAPDVTVAVEETIPSTGRSPNH 283

RESULT 11
 W12659

ID W12659 standard; Protein; 283 AA.

XX W12659;

XX 07-MAY-1997 (first entry)

XX Human herpes simplex virus cellular mediator.

XX Herpes simplex virus cellular mediator; HHEM; receptor; HSV;

XX diagnosis; agonist; antagonist; antibody.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..38

XX Protein 39..283

XX Region 42..75

XX Region 76..120

XX Region 121..162

XX Region 163..185

XX Region 203..225

XX Modified-site 110..112

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

Query Match 99.5%; Score 1570; DB 18; Length 283;
 Best Local Similarity 99.3%; Pred. No. 1.5e-120;
 Matches 281; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPWNRSTPRTDVLRLVLYLFTLGAPCYAPALPSCKEDXPVSGCCPKCSG 60
 D 1 meppgdmgppwnrstprtldvrlrlvlyltflgapyapalpckedexyvgseccpkcspg 60
 QY 61 YVRKACGELGTVCCECPPTGYIAHLNGLSKCIQCCMCBPAKLRNRCSRTENAVCG 120
 D 61 yvrkacgeltgtvcecpptgyiahnglskclqccmcbpamglratncstenaavcg 120
 QY 121 CSPHFCIVODGDHCACRAVATSSPGQRYOKGGTESODTLCONCPGTFSPNGTLEECQ 180
 D 121 cspghfcivodgdhcaacrryatspgqrvqkgtesqdlcqnccpptsngtleecq 180
 QY 181 HQTKCSMLVTRKAGAGTSSHMMWFLSGSLVIVVCSVGLICVRRKRRGADVVKYIVS 240
 D 181 hqtkcsmlvtrkagagtssshmmwflsgslvivvcsvlglicvkrkrkrgadvvkylvs 240
 QY 241 VQKRQAEAGEATVIEALQAPPDVTVAVETIPSTFGSRPNH 283
 D 241 vqkrqaeageatviealqappdvtlvaveetlpsftgrspnh 283

RESULT 12
 Y05797
 ID Y05797 standard; Protein; 283 AA.
 AC Y05797;
 DF 02-AUG-1999 (first entry)
 DE Herpes virus entry mediator (HVEM).
 DX Herpes virus entry mediator; HVEM; HSV receptor; infection;
 KM diagnosis; therapy; vaccine; antiviral; assay.
 OS Human herpes simplex virus.
 PN WO9920761-A2.
 PD 29-APR-1999.
 PF 22-OCT-1998; 98WO-US22342.
 PR 22-OCT-1997; 97US-0955531.
 PA (UNMI) UNIV MICHIGAN.
 PI Fuller AO, Li Q, McLaren NC, Perez A, Subramanian G;
 DR WPI; 1999-302740/25.
 DR N-PSDB; X25512.
 PT Human herpes simplex virus receptor B5 and HVEM compositions
 PS Claim 10; Page 71-72; 89pp; English.
 CC The present sequence represents HVEM, a novel human herpes simplex virus (HSV) entry mediator that is a member of the tumour necrosis factor receptor family, and which confers on HSV the ability to infect and replicate in otherwise non-permissive cells. In the present invention, the combination of a novel porcine cell model system which is refractory to HCV entry, along with specific HSV B5 (see Y05796) and/or HVEM receptor proteins enables the development of assays for screening antiviral compounds and therapeutics. The CC assays are useful for detecting the ability of agents to inhibit HSV entry or spread and provide for facile high-throughput screening of compounds suspected to be able to inhibit such entry, e.g. compound libraries, peptide libraries etc., to identify

CC potential drug candidates. The invention also provides a vaccine comprising the HSV receptor, an immunogenic polypeptide or CC fragments of the polypeptide.
 XX
 SQ Sequence 283 AA;

Query Match 99.5%; Score 1570; DB 20; Length 283;
 Best Local Similarity 99.3%; Pred. No. 1.5e-120;
 Matches 281; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPWNRSTPRTDVLRLVLYLFTLGAPCYAPALPSCKEDXPVSGCCPKCSG 60
 D 1 meppgdmgppwnrstprtldvrlrlvlyltflgapyapalpckedexyvgseccpkcspg 60
 QY 61 YVRKACGELGTVCCECPPTGYIAHLNGLSKCIQCCMCBPAKLRNRCSRTENAVCG 120
 D 61 yvrkacgeltgtvcecpptgyiahnglskclqccmcbpamglratncstenaavcg 120
 QY 121 CSPHFCIVODGDHCACRAVATSSPGQRYOKGGTESODTLCONCPGTFSPNGTLEECQ 180
 D 121 cspghfcivodgdhcaacrryatspgqrvqkgtesqdlcqnccpptsngtleecq 180
 QY 181 HQTKCSMLVTRKAGAGTSSHMMWFLSGSLVIVVCSVGLICVRRKRRGADVVKYIVS 240
 D 181 hqtkcsmlvtrkagagtssshmmwflsgslvivvcsvlglicvkrkrkrgadvvkylvs 240
 QY 241 VQKRQAEAGEATVIEALQAPPDVTVAVETIPSTFGSRPNH 283
 D 241 vqkrqaeageatviealqappdvtlvaveetlpsftgrspnh 283

RESULT 13
 Y79207
 ID Y79207 standard; Protein; 277 AA.
 AC Y79207;
 DF 19-JUN-2000 (first entry)
 DE Membrane-bound herpesvirus entry mediator-2 (mHVEM2).
 DX mHVEM-2; membrane-bound herpesvirus entry mediator-2;
 KM TANGO-69-receptor; tumour necrosis factor receptor; human;
 KM herpes simplex virus; infection; cancer; inflammation;
 OS auto-immune disorder; therapy; diagnosis.
 OS Homo sapiens.
 FH Key
 FH Peptide
 FT /note="signal peptide"
 FT /note="mature protein, also separately claimed in Claim 8"
 FT Domain
 FT /note="cysteine-rich domain"
 FT /note="cysteine-rich domain"
 FT /note="cysteine-rich domain"
 FT /note="cysteine-rich domain (partial)"
 FT Domain
 FT /note="transmembrane domain"
 FT /note="N-glycosylated"
 FT /note="N-glycosylated"
 FT /note="N-glycosylated"
 FT /note="N-glycosylated"
 PN WO200014230-A1.
 PD 16-MAR-2000.

XX 03-SEP-1999; 99WO-US20180.
 PF 03-SEP-1998; 98US-0146950.
 PR 29-JUN-1999; 99US-0342767.
 XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX
 PI Busfield SJ;
 PI WPI: 2000-256981/22.
 DR N-PSDB; 294198.
 DR
 XX
 PT New nucleic acid molecule encoding herpes virus entry mediator (HVEM),
 PT either in the soluble or membrane bound form, is useful in screening
 PT assays and detection assays -
 XX
 PS Claim 8; Fig 7; 149pp; English.
 XX
 CC This polypeptide, the mature portion of which is also claimed,
 CC is human membrane-bound herpesvirus entry mediator-2 (mhVEM2); a
 CC novel form of membrane-bound herpesvirus entry mediator (mhVEM).
 CC The amino acid sequence was deduced from an isolated cDNA clone
 CC (see 294198). mhVEM2 is a TANGO-69-receptor and member of the
 CC tumour necrosis factor receptor (TNFR) superfamily. HVEM plays a
 CC role in herpes simplex virus (HSV) entry. The invention is based
 CC on the discovery of 3 cDNA molecules (see 294195-97) which encode
 CC soluble forms (see Y79204-06) of mhVEM, and the cDNA molecule
 CC encoding of mhVEM2. In addition to isolated full-length proteins
 CC and polynucleotides, and invention provides TANGO-69-receptor
 CC fusion proteins, antigenic peptides and antibodies. Also provided
 CC are recombinant expression vectors, host cells and transgenic
 CC animals in which a TANGO-69-receptor gene has been introduced or
 CC disrupted. DNA encoding HVEM, HVEM proteins and HVEM antibodies
 CC can be used in screening and detection assays (e.g. chromosomal
 CC mapping, tissue typing). HVEM proteins can also be used for
 CC regulation of cell proliferation, cell differentiation, cell
 CC survival, inflammation mast cell activity, HSV infection and/or
 CC proliferation, and/or coagulation. HVEM agonists can be used to
 CC treat disorders associated with decreased HVEM activity, e.g.
 CC proliferative disorders such as carcinoma or pathogenic infection.
 CC Antagonists can be used to treat disorders associated with
 CC increased HVEM activity, e.g. autoimmune, T cell, inflammatory and
 CC allergic inflammation disorders.
 CC
 XX
 XX Sequence 277 AA:
 Query Match 87.0%; Score 1373.5; DB 21; Length 277;
 Best Local Similarity 93.5%; Pred. No. 1.6e-104;
 Matches 245; Conservative 2; Mismatches 6; Indels 9; Gaps 1;
 QY 1 MEPPGDMGPPMRSTPRTDYLRLVLTFTFGACYAPALPSCKEDEVPSSECCPKSPG 60
 DB 1 meppgdmgppmrstprtldvrlvltftfgacyapalpsckedevpssecpkspg 60
 QY 61 YRVVACGELTGTCEPCPGTYIAHNGSKLCOCMCPANGLRNRCSSTENAVCG 120
 DB 61 yrvvacaageltgtvcepcpgtyiahngsklccqcmcpanglrsrncstenaavcg 120
 QY 121 CSPGHCFIVODGHCACRAVATSSPGQROVKGSTESQDTLCONCPGTFSPNGTLEECQ 180
 DB 121 cspghcfivodgdhcaacraavatsspgqrovkgstesqdtlcnpcpgtfsngtleecq 180
 QY 181 HQRKCSMLYTKAGAGTSSSHWMMFLSGSLVITYVCTVLLICVRRKRGDVVKYIVS 240
 DB 181 hqkcsmlvtkagagtssshwmmflsgslvityvctvllicvrrkrgdvvkivys 240
 QY 241 VQRKROEAGEATVTEALQAP 262
 DB 241 vq-----vlllplslp 253

RESULT 14
 ID Y79204
 XX Y79204 standard; Protein; 193 AA.
 AC Y79204;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Soluble herpesvirus entry mediator-1 (SHVEM1).
 XX
 KW SHVEM-1; soluble herpesvirus entry mediator-1; TANGO-69-receptor;
 KW tumour necrosis factor receptor; human; herpes simplex virus;
 KW infection; cancer; inflammation; autoimmune disorder; therapy;
 KW diagnosis.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..36
 FT /note= "signal peptide"
 FT Protein 37..193
 FT /note= "mature protein, also separately claimed
 FT in Claim 8"
 FT Domain 42..75
 FT /note= "cysteine-rich domain"
 FT Domain 78..119
 FT /note= "cysteine-rich domain"
 FT Domain 121..162
 FT /note= "cysteine-rich domain"
 FT Modified-site 110
 FT /note= "N-glycosylated"
 FT Modified-site 173
 FT /note= "N-glycosylated"
 FT
 XX WO200014230-A1.
 XX 16-MAR-2000.
 PD
 XX
 PF 03-SEP-1999; 99WO-US20180.
 XX
 PR 03-SEP-1998; 98US-0146950.
 PR 29-JUN-1999; 99US-0342767.
 XX
 XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 PA
 PI Busfield SJ;
 PI WPI: 2000-256981/22.
 DR N-PSDB; 294195.
 DR
 XX
 PT New nucleic acid molecule encoding herpes virus entry mediator (HVEM),
 PT either in the soluble or membrane bound form, is useful in screening
 PT assays and detection assays -
 XX
 XX Claim 8; Fig 1; 149pp; English.
 XX
 CC This polypeptide, the mature portion of which is also claimed,
 CC is human soluble herpesvirus entry mediator-1 (SHVEM1), a novel
 CC soluble form of membrane-bound herpesvirus entry mediator (mhVEM).
 CC The amino acid sequence was deduced from an isolated cDNA clone
 CC (see 294195). SHVEM1 is a TANGO-69-receptor and member of the
 CC tumour necrosis factor receptor (TNFR) superfamily. It is
 CC thought to play a role analogous to other soluble members of the
 CC TNFR superfamily by interfering with the ability of LIGHT-TANGO-69
 CC and lymphotoxin to bind mhVEM, and to play a role in herpes simplex
 CC virus (HSV) entry. The invention is based on the discovery of 3
 CC cDNA molecules (see 294195-97) which encode soluble forms (see
 CC Y79204-06), and 1 cDNA molecule (see 294198) that encodes a 2nd
 CC membrane-bound form (see Y79207), of mhVEM. In addition to
 CC isolated full-length proteins and polynucleotides, and invention
 CC provides TANGO-69-receptor fusion proteins, antigenic peptides and
 CC antibodies. Also provided are recombinant expression vectors,
 CC host cells and transgenic animals in which a TANGO-69-receptor

CC gene has been introduced or disrupted. DNA encoding HVEM, HVEM
 CC proteins and HVEM antibodies can be used in screening and detection
 CC assays (e.g. chromosomal mapping, tissue typing). HVEM proteins
 CC can also be used for regulation of cell proliferation, cell
 CC differentiation, cell survival, inflammation mast cell activity,
 CC HSV infection and/or proliferation, and/or coagulation. HVEM
 CC agonists can be used to treat disorders associated with decreased
 CC HVEM activity, e.g. proliferative disorders such as carcinoma or
 CC pathogenic infection. Antagonists can be used to treat disorders
 CC associated with increased HVEM activity, e.g. autoimmune, T cell,
 CC inflammatory and allergic inflammation disorders.

XX
 SQ Sequence 193 AA:

Query Match 67.7%; Score 1068; DB 21; Length 193;
 Best Local Similarity 98.4%; Pred. No. 8.6e-80;
 Matches 184; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MEPPDGMGPPWRSTPRDVLRLVLYLFLGAPCYAPALPSCKEDEYVSGSECCPKCSPG 60
 DB 1 MEPPDGMGPPWRSTPRDVLRLVLYLFLGAPCYAPALPSCKEDEYVSGSECCPKCSPG 60
 OY 61 YRVKACGELTGTCVCEPCPGTYIAHLNGLSKLCQCMCDPAMGIRASRNCSTENAVCG 120
 DB 61 YRVKACGELTGTCVCEPCPGTYIAHLNGLSKLCQCMCDPAMGIRASRNCSTENAVCG 120
 OY 121 CSPGHFCIVDGDHCAACRAATSSPGRVKGGTESDITLCQNCPTGFSPNGLTECCQ 180
 DB 121 CSPGHFCIVDGDHCAACRAATSSPGRVKGGTESDITLCQNCPTGFSPNGLTECCQ 180
 OY 181 HQTCKSW 187
 DB 181 hqtnraw 187

RESULT 15
 ID Y79205
 Y79205 standard; Protein; 197 AA.

XX AC Y79205;
 XX 19-JUN-2000 (first entry)
 DE Soluble herpesvirus entry mediator-2 (SHVEM2).
 XX
 KM SHVEM-2; soluble herpesvirus entry mediator-2; TANGO-69-receptor;
 KM tumour necrosis factor receptor; human; herpes simplex virus;
 KW infection; cancer; inflammation; autoimmune disorder; therapy;
 KW diagnosis.

XX Homo sapiens.

XX FH Key Location/Qualifiers
 FT Peptide 1..38
 FT /note= "signal peptide"
 FT Protein 39..197
 FT /note= "mature protein, also separately claimed
 FT in Claim 8"
 FT Domain 42..75
 FT /note= "cysteine-rich domain"
 FT Domain 78..119
 FT /note= "cysteine-rich domain"
 FT Domain 121..162
 FT /note= "cysteine-rich domain"
 FT Modified-site 110
 FT /note= "N-glycosylated"
 FT Modified-site 173
 FT /note= "N-glycosylated"

XX WO200014230-A1.
 XX 16-MAR-2000.

XX 03-SEP-1999; 99WO-US20180.
 XX 03-SEP-1998; 98US-0146950.
 PR 29-JUN-1999; 99US-0342767.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

PI Busfield SJ;

XX WPI: 2000-256981/22.

DR N-PSDB: 294196.

PT New nucleic acid molecule encoding herpes virus entry mediator (HVEM),
 PT either in the soluble or membrane bound form, is useful in screening
 PT assays and detection assays -

PS Claim 8; Fig 3; 149pp; English.

CC This polypeptide, the mature portion of which is also claimed,
 CC is human soluble herpesvirus entry mediator-2 (SHVEM2), a novel
 CC soluble form of membrane-bound herpesvirus entry mediator (mHVEM).
 CC The amino acid sequence was deduced from an isolated cDNA clone
 CC (see 294196). SHVEM2 is a TANGO-69-receptor and member of the
 CC tumour necrosis factor receptor (TNFR) superfamily. It is
 CC thought to play a role analogous to other soluble members of the
 CC TNFR superfamily by interfering with the ability of LIGHT-TANGO-69
 CC and lymphotoxin to bind mHVEM, and to play a role in herpes simplex
 CC virus (HSV) entry. The invention is based on the discovery of 3
 CC cDNA molecules (see 294195-97) which encode soluble forms (see
 CC Y79204-06), and 1 cDNA molecule (see 294198) that encodes a 2nd
 CC membrane-bound form (see Y79207), of mHVEM. In addition to
 CC isolated full-length proteins and polynucleotides, and invention
 CC provides TANGO-69-receptor fusion proteins, antigenic peptides and
 CC antibodies. Also provided are recombinant expression vectors,
 CC host cells and transgenic animals in which a TANGO-69-receptor
 CC gene has been introduced or disrupted. DNA encoding HVEM, HVEM
 CC proteins and HVEM antibodies can be used in screening and detection
 CC assays (e.g. chromosomal mapping, tissue typing). HVEM proteins
 CC can also be used for regulation of cell proliferation, cell
 CC differentiation, cell survival, inflammation mast cell activity,
 CC HSV infection and/or proliferation, and/or coagulation. HVEM
 CC agonists can be used to treat disorders associated with decreased
 CC HVEM activity, e.g. proliferative disorders such as carcinoma or
 CC pathogenic infection. Antagonists can be used to treat disorders
 CC associated with increased HVEM activity, e.g. autoimmune, T cell,
 CC inflammatory and allergic inflammation disorders.

SQ Sequence 197 AA;

Query Match 67.2%; Score 1060; DB 21; Length 197;
 Best Local Similarity 98.4%; Pred. No. 4e-79;
 Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

OY 1 MEPPDGMGPPWRSTPRDVLRLVLYLFLGAPCYAPALPSCKEDEYVSGSECCPKCSPG 60
 DB 1 MEPPDGMGPPWRSTPRDVLRLVLYLFLGAPCYAPALPSCKEDEYVSGSECCPKCSPG 60
 OY 61 YRVKACGELTGTCVCEPCPGTYIAHLNGLSKLCQCMCDPAMGIRASRNCSTENAVCG 120
 DB 61 YRVKACGELTGTCVCEPCPGTYIAHLNGLSKLCQCMCDPAMGIRASRNCSTENAVCG 120
 OY 121 CSPGHFCIVDGDHCAACRAATSSPGRVKGGTESDITLCQNCPTGFSPNGLTECCQ 180
 DB 121 CSPGHFCIVDGDHCAACRAATSSPGRVKGGTESDITLCQNCPTGFSPNGLTECCQ 180
 OY 181 HQTCKSW 187
 DB 181 hqt--nw 185

Wed Apr 25 17:48:12 2001

us-08-741-095b-26.rag

Page 12

Search completed: April 25, 2001, 17:34:32
Job time: 173 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 25, 2001, 17:34:14 ; Search time 22.97 Seconds
(without alignments)
1444.050 Million cell updates/sec

Title: US-08-741-095b-26
Perfect score: 1578
Sequence: 1 MEPPGDMGPPMRSTPRTDV.....VTVAVETIPSTGRSPNH 283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_15:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhnc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_unclassified:*
14: sp_vertebrate:*
14: sp_virus:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1578	100.0	283	4 Q92956	Q92956 homo sapien
2	1578	99.8	283	4 Q9UM65	Q9UM65 homo sapien
3	1303.5	82.6	283	6 Q9XS28	Q9XS28 cercopithec
4	271.5	17.2	349	14 Q57100	Q57100 monkeypox v
5	269.5	17.1	348	14 Q57277	Q57277 monkeypox v
6	269.5	17.1	348	14 Q57108	Q57108 monkeypox v
7	269.5	17.1	349	14 Q57291	Q57291 monkeypox v
8	269.5	17.1	349	14 Q57101	Q57101 monkeypox v
9	269.5	17.1	349	14 Q57102	Q57102 monkeypox v
10	266.5	16.9	349	14 Q57284	Q57284 camelpox vi
11	266.5	16.9	349	14 Q57098	Q57098 camelpox vi
12	265.5	16.8	348	14 Q57103	Q57103 monkeypox v
13	265.5	16.8	349	14 Q57099	Q57099 monkeypox v
14	262.5	16.6	349	14 Q57097	Q57097 camelpox vi
15	259	16.4	349	14 Q57111	Q57111 variola vir
16	259	16.4	439	4 Q16042	Q16042 homo sapien
17	257.5	16.3	348	14 Q57112	Q57112 variola vir
18	257.5	16.3	348	14 Q85407	Q85407 variola vir
19	257.5	16.3	351	14 Q57117	Q57117 cowpox viru

20	257	16.3	349	14 Q57110	Q57110 variola vir
21	257	16.3	349	14 Q89118	Q89118 variola vir
22	257	16.3	349	14 Q89098	Q89098 variola vir
23	249	15.8	349	14 Q57109	Q57109 variola vir
24	246	15.6	300	4 Q95407	Q95407 homo sapien
25	243.5	15.4	351	14 Q73559	Q73559 cowpox viru
26	239	15.1	350	14 Q57116	Q57116 cowpox viru
27	236.5	15.0	351	14 Q57121	Q57121 cowpox viru
28	232.5	14.7	349	14 Q57305	Q57305 cowpox viru
29	229.5	14.5	349	14 Q57122	Q57122 cowpox viru
30	229	14.5	347	14 Q57119	Q57119 cowpox viru
31	228.5	14.5	326	14 Q57120	Q57120 cowpox viru
32	228	14.4	360	14 Q57118	Q57118 cowpox viru
33	226.5	14.4	350	14 Q57123	Q57123 cowpox viru
34	225.5	14.3	347	14 Q57115	Q57115 cowpox viru
35	225.5	14.3	355	14 Q85308	Q85308 cowpox viru
36	219.5	13.9	267	6 Q02764	Q02764 oryctolagus
37	219.5	13.9	319	6 Q9TV79	Q9TV79 oryctolagus
38	218	13.8	320	6 Q9XS29	Q9XS29 oryctolagus
39	215.5	13.7	263	6 Q9XS60	Q9XS60 oryctolagus
40	213.5	13.5	320	14 Q57079	Q57079 cowpox viru
41	213.5	13.5	417	11 Q9Z0W1	Q9Z0W1 mus muscu
42	212.5	13.5	459	11 Q62327	Q62327 mus muscu
43	212	13.4	320	14 Q57091	Q57091 ectromelia
44	212	13.4	320	14 Q57300	Q57300 ectromelia
45	210	13.3	372	4 Q9UHP4	Q9UHP4 homo sapien

ALIGNMENTS

RESULT 1
ID Q92956 PRELIMINARY; PRT; 283 AA.

AC Q92956;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HERPESVIRUS ENTRY MEDIATOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97053782; PubMed=8898196;
RA Montomery R.L., Warner M.S., Lum B.J., Spear P.G.;
RT "Herpes simplex virus-1 entry into cells mediated by a novel member of
the TNF/NGF receptor family.";
RL Cell 87:427-436(1996).
DR EMBL: U70321; AAB58354.1; -;
DR HSSP: P25942; 1CDF.
DR INTERPRO: IPR001368; -;
DR PFAM: PF00020; TNFR_C6; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
DR PRODOM: PD000771; -; 1.
SQ SEQUENCE 283 AA; 30420 MW; DFCFI46E4ED024F4B CRC64;

Query Match 100.0%; Score 1578; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 26-143;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMRSTPRTDVRLVLYLTETIGAPCYAPALPSCKEDYPPVSGCCPKCSFG 60
|||||
QY 1 MEPPGDMGPPMRSTPRTDVRLVLYLTETIGAPCYAPALPSCKEDYPPVSGCCPKCSFG 60
|||||
QY 61 YRKEACGELTGVCCECPGPTTAHNGLSKICQCCMPAMGLRNRCSRTENAVCG 120
|||||
QY 61 YRKEACGELTGVCCECPGPTTAHNGLSKICQCCMPAMGLRNRCSRTENAVCG 120
|||||
QY 121 CSPGHFCIVDDGHCACACRAVATSSPGORVOKGCTESQDTLCONCPGTFSPNGLTECCQ 180
|||||

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Db 121 CSPGHFCIYVDDGHCAACRAVATSSPGQRYOKGTESDTLCONCPGTFSPNGTLEECQ 180
181 HQTCKSWLTKAGAGTSSSHWMMFLSGSLVIYIVCSTVGLITCKVRRKRGDVKVIVS 240
181 HQTCKSWLTKAGAGTSSSHWMMFLSGSLVIYIVCSTVGLITCKVRRKRGDVKVIVS 240
QY 241 VQRRKQAEAGEATVIALQAPPDVTVAVEETIPSTFGSRPNH 283
Db 241 VQRRKQAEAGEATVIALQAPPDVTVAVEETIPSTFGSRPNH 283

RESULT 2
Q9DM65 PRELIMINARY; PRT; 283 AA.
ID 09DM65
AC 09DM65;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR-LIKE GENE 2 (CD40-LIKE PROTEIN
DE PRECURSOR).
GN TR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kwon B.S., Tan K.B., Ni J.;
RT "A newly-identified member of the tumor necrosis factor receptor
RT superfamily with a wide tissue distribution and involvement in
RT lymphocyte activation."
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., Cao X.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U01232; AAD00505.1;
DR EMBL; AF153978; AAF75588.1;
DR HSSP; P25942; ICDF.
DR INTERPRO; IPR001368;
DR PFAM; PF00020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 283 AA; 30392 MW; 46CF13C2C70242C1 CRC64;

Query Match 99.8%; Score 1575; DB 4; Length 283;
Best Local Similarity 99.6%; Pred. No. 3.9e-143;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPPGDMGPPMWRSTPRTDVLRLVLTFLGACVAPALPSCKEDEYPVGSECCPRKSPG 60
Db 1 MEPPGDMGPPMWRSTPRTDVLRLVLTFLGACVAPALPSCKEDEYPVGSECCPRKSPG 60
QY 61 YRKKEAGELTGVCEPCPGTYIAHLNGLSKLQCOMCDPAGLRSRNCSTENAVCG 120
Db 61 YRKKEAGELTGVCEPCPGTYIAHLNGLSKLQCOMCDPAGLRSRNCSTENAVCG 120
QY 121 CSGHFCIYVDDGHCAACRAVATSSPGQRYOKGTESDTLCONCPGTFSPNGTLEECQ 180
Db 121 CSGHFCIYVDDGHCAACRAVATSSPGQRYOKGTESDTLCONCPGTFSPNGTLEECQ 180
QY 181 HQTCKSWLTKAGAGTSSSHWMMFLSGSLVIYIVCSTVGLITCKVRRKRGDVKVIVS 240
Db 181 HQTCKSWLTKAGAGTSSSHWMMFLSGSLVIYIVCSTVGLITCKVRRKRGDVKVIVS 240
QY 241 VQRRKQAEAGEATVIALQAPPDVTVAVEETIPSTFGSRPNH 283
Db 241 VQRRKQAEAGEATVIALQAPPDVTVAVEETIPSTFGSRPNH 283

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RESULT 3
Q9XS28 PRELIMINARY; PRT; 283 AA.
ID 09XS28
AC 09XS28;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HVEAS.
GN HVEAS.
OS Cercopithecus aethiops (Green monkey) (Griwet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciae;
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=99296730; PubMed=10366573;
RA Foster T.P., Choujengo V.N., Kousoulas K.G.;
RT "Functional characterization of the HveA homolog specified by African
RT green monkey kidney cells with a herpes simplex virus expressing the
RT green fluorescence protein."
RL Virology 258:365-374(1999).
DR EMBL; AF147720; AAD37381.1;
DR HSSP; P25942; ICDF.
DR INTERPRO; IPR001368;
DR PFAM; PF00020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
SQ SEQUENCE 283 AA; 30199 MW; 397951C6617FE3AA CRC64;

Query Match 82.6%; Score 1303.5; DB 6; Length 283;
Best Local Similarity 82.0%; Pred. No. 4.1e-117;
Matches 232; Conservative 18; Mismatches 30; Indels 3; Gaps 2;
QY 1 MEPPGDMGPPMWRSTPRTDVLRLVLTFLGACVAPALPSCKEDEYPVGSECCPRKSPG 60
Db 1 MEPPGDMGPPMWRSTPRTDVLRLVLTFLGSSCYAPALPSCKEDEYPVGSECCPRKSPG 60
QY 61 YRKKEAGELTGVCEPCPGTYIAHLNGLSKLQCOMCDPAGLRSRNCSTENAVCG 120
Db 61 FHVROAGGEQGTGVCEPCPGTYIAHLNGLSKLQCOMCDPAGLRSRNCSTENAVCG 120
QY 121 CSGHFCIYVDDGHCAACRAVATSSPGQRYOKGTESDTLCONCPGTFSPNGTLEECQ 180
Db 121 CSGHFCIYVDDGHCAACRAVATSSPGQRYOKGTESDTLCONCPGTFSPNGTLEECQ 180
QY 181 HQTCKSWLTKAGAGTSSSHWMMFLSGSLVIYIVCSTV--GLITCKVRRKRGDVKV 237
Db 181 HQTCKSWLTKAGAGTSSSHWMMFLSGSLVIYIVCSTV--GLITCKVRRKRGDVKV 237
QY 238 IVSVQRRKQAEAGEATVIALQAPPDVTVAVEETIPSTFGSR 280
Db 241 IVSVQRRKQAEAGEATVIALQAPPDVTVAVEETIPSTFGSR 283

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RESULT 4
O57100 PRELIMINARY; PRT; 349 AA.
ID 057100
AC 057100;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIGERIA-1971 (71-0082);

```


RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U87844; AAB94361.1; -
 DR HSSP: P25942; ICDF.
 DR INTERPRO: IPR001368; -
 DR PRAM: PF00020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SO SEQUENCE 349 AA; 38239 MW; DE6C280D478F2422 CRC64;

Query Match 17.2%; Score 271.5; DB 14; Length 349;
 Best Local Similarity 32.6%; Pred. No. 3.9e-18;
 Matches 59; Conservative 23; Mismatches 80; Indels 19; Gaps 5;

OY 21 LRLVLYLFLGAPC-----YAPALPCKDEYVSGCCPKSPGYRVEACGEL 70
 DB 1 MRSVLYSYILFLSCIINGRDIAPHAPNSGCKDNERSRNLCCLSCPPGTYASRLCDISK 60
 OY 71 TGVCEPCPPGTIYAHNGLSKLCLOCO-MCDPAMGLRASRNCSTENAVCGCSPGHFCIV 129
 DB 61 TNNCTCGSGDTFTSHNHQACLSGNCRCDSNOVETRSCNTHNRICCSGTYCL 118
 OY 130 QGDGHCAACRAVATSSPGQRYVGKGTESQDTLCONCPGTFSPNGTLEECQHQTCSMTLV 189
 DB 119 KGSGGCTCISKTGCGIGYGV-SGYTSTGDIVICSPCGGTYS-----HTVSTDKCEPV 172
 OY 190 T 190
 DB 173 T 173

RESULT 5
 O57277 PRELIMINARY; PRT; 348 AA.
 AC O57277;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRMB.
 OS Monkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Zaire-1996(96-17), Zaire-1996 (96-16);
 RL Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U88543; AAB94378.1; -
 DR EMBL: U87841; AAB94358.1; -
 DR HSSP: P25942; ICDF.
 DR INTERPRO: IPR001368; -
 DR PRAM: PF00020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SO SEQUENCE 348 AA; 38212 MW; 54019521556C2DBF CRC64;

Query Match 17.1%; Score 269.5; DB 14; Length 348;
 Best Local Similarity 32.6%; Pred. No. 6e-18;
 Matches 57; Conservative 25; Mismatches 78; Indels 15; Gaps 5;

OY 21 LRLVLYLFLGAPC-----YAPALPCKDEYVSGCCPKSPGYRVEACGEL 70
 DB 1 MRSVLYSYILFLSCIINGRDIAPHAPNSGCKDNERSRNLCCLSCPPGTYASRLCDISK 60
 OY 71 TGVCEPCPPGTIYAHNGLSKLCLOCO-MCDPAMGLRASRNCSTENAVCGCSGHCIV 129
 DB 61 TNNCTCGSGDTFTSHNHQACLSGNCRCDSNOVETRSCNTHNRICCSGTYCL 118

OY 130 QGDGHCAACRAVATSSPGQRYVGKGTESQDTLCONCPGTFSPN-GTLEECQHQT 183
 DB 119 KGSGGCTCISKTGCGIGYGV-SGYTSTGDIVICSPCGGTYSHTVSTDKCEPV 172

RESULT 6
 O57108 PRELIMINARY; PRT; 348 AA.
 ID O57108;
 AC O57108;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRMB.
 OS Monkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Zaire-1970 (CONGO-8);
 RL Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U88142; AAB94367.1; -
 DR HSSP: P25942; ICDF.
 DR INTERPRO: IPR001368; -
 DR PRAM: PF00020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SO SEQUENCE 348 AA; 38212 MW; E55979057DEC91F CRC64;

Query Match 17.1%; Score 269.5; DB 14; Length 348;
 Best Local Similarity 32.6%; Pred. No. 6e-18;
 Matches 57; Conservative 25; Mismatches 78; Indels 15; Gaps 5;

OY 21 LRLVLYLFLGAPC-----YAPALPCKDEYVSGCCPKSPGYRVEACGEL 70
 DB 1 MRSVLYSYILFLSCIINGRDIAPHAPNSGCKDNERSRNLCCLSCPPGTYASRLCDISK 60
 OY 71 TGVCEPCPPGTIYAHNGLSKLCLOCO-MCDPAMGLRASRNCSTENAVCGCSPGHFCIV 129
 DB 61 TNNCTCGSGDTFTSHNHQACLSGNCRCDSNOVETRSCNTHNRICCSGTYCL 118
 OY 130 QGDGHCAACRAVATSSPGQRYVGKGTESQDTLCONCPGTFSPN-GTLEECQHQT 183
 DB 119 KGSGGCTCISKTGCGIGYGV-SGYTSTGDIVICSPCGGTYSHTVSTDKCEPV 172

RESULT 7
 O57291 PRELIMINARY; PRT; 349 AA.
 ID O57291;
 AC O57291;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRMB.
 OS Monkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VARIOUS STRAINS;
 RL Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U88144; AAB94368.1; -
 DR EMBL: U87842; AAB94359.1; -
 DR EMBL: U87994; AAB94365.1; -
 DR EMBL: U87995; AAB94366.1; -

DR EMBL: U08143; AAB94368.1; -
 DR HSSP: P25942; 1CDF.
 DR INTERPRO: IPR001368; -
 DR PRAM: PF00020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SQ SEQUENCE 349 AA; 38295 MW; CBD2C949ED2B8E7C CRC64;

Query Match 17.1%; Score 269.5; DB 14; Length 349;
 Best Local Similarity 32.6%; Pred. No. 6e-18;
 Matches 59; Conservative 22; Mismatches 81; Indels 19; Gaps 5;

QY 21 LRLVLYTFGLGAPC-----YAPALPSCKEDEPVGSECCPKSPGYRVKAEAGEL 70
 DB 1 MRSVLYSYILFLSCIIINGNDIAPHASNGCKDNEIRSRNLLCCLCPPTVYASRLCD 60
 QY 71 TGVYCEPCPGPYIAHLNGLSKLCLOCO-MCDPAMGLRASHNCSTENAVAGCSPGHFCIV 129
 DB 61 TMTQCTPCGSDTFTSHNNHQAQCLSCNGRCD--SNQVETRSCTNTHNRICECSPGYCYCL 118
 QY 130 QDDDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQHOTKCSMLV 189
 DB 119 KGASGCRCTISKTKGIGYGV-SGYTSTGDIVICSPCGPGTYS-----HTVSTDKCEPV 172
 QY 190 T 190
 DB 173 T 173

RESULT 8
 057101 PRELIMINARY; PRT; 349 AA.

AC 057101;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRMB.
 OS Monkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OC NCBI_Taxid=10244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ZAIRE-1977 (77-0666);
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U08143; AAB94362.1; -
 DR HSSP: P25942; 1CDF.
 DR INTERPRO: IPR001368; -
 DR PRAM: PF00020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SQ SEQUENCE 349 AA; 38311 MW; 02F65B00CEB858BE CRC64;

Query Match 17.1%; Score 269.5; DB 14; Length 349;
 Best Local Similarity 32.6%; Pred. No. 6e-18;
 Matches 59; Conservative 22; Mismatches 81; Indels 19; Gaps 5;
 QY 21 LRLVLYTFGLGAPC-----YAPALPSCKEDEPVGSECCPKSPGYRVKAEAGEL 70
 DB 1 MRSVLYSYILFLSCIIINGNDIAPHASNGCKDNEIRSRNLLCCLCPPTVYASRLCD 60
 QY 71 TGVYCEPCPGPYIAHLNGLSKLCLOCO-MCDPAMGLRASHNCSTENAVAGCSPGHFCIV 129
 DB 61 TMTQCTPCGSDTFTSHNNHQAQCLSCNGRCD--SNQVETRSCTNTHNRICECSPGYCYCL 118
 QY 130 QDDDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQHOTKCSMLV 189

DB 119 KGASGCRCTISKTKGIGYGV-SGYTSTGDIVICSPCGPGTYS-----HTVSTDKCEPV 172
 QY 190 T 190
 DB 173 T 173

RESULT 9
 057102 PRELIMINARY; PRT; 349 AA.

AC 057102;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRMB.
 OS Monkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OC NCBI_Taxid=10244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BENIN-1978 (78-3945);
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U08146; AAB94363.1; -
 DR HSSP: P25942; 1CDF.
 DR INTERPRO: IPR001368; -
 DR PRAM: PF00020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SQ SEQUENCE 349 AA; 38308 MW; CBD2C949F994C59C CRC64;

Query Match 17.1%; Score 269.5; DB 14; Length 349;
 Best Local Similarity 32.6%; Pred. No. 6e-18;
 Matches 59; Conservative 22; Mismatches 81; Indels 19; Gaps 5;

QY 21 LRLVLYTFGLGAPC-----YAPALPSCKEDEPVGSECCPKSPGYRVKAEAGEL 70
 DB 1 MRSVLYSYILFLSCIIINGNDIAPHASNGCKDNEIRSRNLLCCLCPPTVYASRLCD 60
 QY 71 TGVYCEPCPGPYIAHLNGLSKLCLOCO-MCDPAMGLRASHNCSTENAVAGCSPGHFCIV 129
 DB 61 TMTQCTPCGSDTFTSHNNHQAQCLSCNGRCD--SNQVETRSCTNTHNRICECSPGYCYCL 118
 QY 130 QDDDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQHOTKCSMLV 189
 DB 119 KGASGCRCTISKTKGIGYGV-SGYTSTGDIVICSPCGPGTYS-----HTVSTDKCEPV 172
 QY 190 T 190
 DB 173 T 173

RESULT 10
 057284 PRELIMINARY; PRT; 349 AA.

AC 057284;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRMB.
 OS Camelipox virus (strain CP-1).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OC NCBI_Taxid=28873;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DUBAI-1992 (CP-5), SOMALIA-1978;
 RA Loparev V.N., Parsons J.M., Esposito J.J.;

Submitted (Jan-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL: U87840; AAB94357.1; -
 DR EMBL: U87837; AAB94354.1; -
 DR HSSP: P25942; ICDF.
 DR INTERPRO: IPR001368; -
 DR PFAM: PF00020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SQ SEQUENCE 349 AA; 38036 MW; EA412AE86E090E4 CRC64;

Query Match 16.9%; Score 266.5; DB 14; Length 349;
 Best Local Similarity 33.1%; Pred. No. 1.2e-17;
 Matches 57; Conservative 24; Mismatches 76; Indels 15; Gaps 5;

OY 21 LRLVLYLFLAPC-----YAPALPSCKDEYVSGCCPKSPGYRVKACGEL 70.
 Db 1 MKSVLYSTLLSCIIINGRDVTPAPNSGCKDNEYRHHNLCCISCPPGTYASRLCDCK 60
 OY 71 TGVCEPCPGTYIAHLNGLSKLCQO-MCDPAMGLRASRNCSTENAVCGSPGHFCIV 129
 Db 61 TINTCTPGSGSTFTSRNHLPLACLSGNCGRD--SNQVETRSCNTHNHRICSGSGYICIL 118
 OY 130 QDGHCAACRAVATSSPGQRYOKGTESDPTLCONCPPGTSPN-GTLEECQ 180
 Db 119 KSSGCKACVSGTCKGIGYV-SGHTSAGDVICSPCGIGTYSRTVSSADKCE 169

RESULT 11

057098 ID 057098 PRELIMINARY; PRT; 349 AA.

AC 057098;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRMB.
 OS Camelpox virus (strain CP-1).
 OC Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 CC Orthopoxvirus.
 OX NCBI_TaxID=28873;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-SAUDI-M3;
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (Jan-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U87839; AAB94356.1; -
 DR HSSP: P25942; ICDF.
 DR INTERPRO: IPR001368; -
 DR PFAM: PF00020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SQ SEQUENCE 349 AA; 37978 MW; 8630EFAED7A584B5 CRC64;

Query Match 16.9%; Score 266.5; DB 14; Length 349;
 Best Local Similarity 33.1%; Pred. No. 1.2e-17;
 Matches 57; Conservative 24; Mismatches 76; Indels 15; Gaps 5;

OY 21 LRLVLYLFLAPC-----YAPALPSCKDEYVSGCCPKSPGYRVKACGEL 70
 Db 1 MKSVLYSTLLSCIIINGRDVTPAPNSGCKDNEYRHHNLCCISCPPGTYASRLCDCK 60
 OY 71 TGVCEPCPGTYIAHLNGLSKLCQO-MCDPAMGLRASRNCSTENAVCGSPGHFCIV 129
 Db 61 TINTCTPGSGSTFTSRNHLPLACLSGNCGRD--SNQVETRSCNTHNHRICSGSGYICIL 118
 OY 130 QDGHCAACRAVATSSPGQRYOKGTESDPTLCONCPPGTSPN-GTLEECQ 180
 Db 119 KSSGCKACVSGTCKGIGYV-SGHTSAGDVICSPCGIGTYSRTVSSADKCE 169

RESULT 12

057103 ID 057103 PRELIMINARY; PRT; 348 AA.

AC 057103;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRMB.
 OS Monkeypox virus.
 OC Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 CC Orthopoxvirus.
 OX NCBI_TaxID=10244;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-ZAIRE-1979 (79-0005);
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (Jan-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U87847; AAB94364.1; -
 DR HSSP: P25942; ICDF.
 DR INTERPRO: IPR001368; -
 DR PFAM: PF00020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SQ SEQUENCE 348 AA; 38184 MW; 34A5E68B27907B5 CRC64;

Query Match 16.8%; Score 265.5; DB 14; Length 348;
 Best Local Similarity 32.0%; Pred. No. 1.4e-17;
 Matches 56; Conservative 25; Mismatches 79; Indels 15; Gaps 5;

OY 21 LRLVLYLFLAPC-----YAPALPSCKDEYVSGCCPKSPGYRVKACGEL 70
 Db 1 MRSALYSTLLSCIIINGRDVTPAPNSGCKDNEYRHHNLCCISCPPGTYASRLCDCK 60
 OY 71 TGVCEPCPGTYIAHLNGLSKLCQO-MCDPAMGLRASRNCSTENAVCGSPGHFCIV 129
 Db 61 TINTCTPGSGSTFTSRNHLPLACLSGNCGRD--SNQVETRSCNTHNHRICSGSGYICIL 118
 OY 130 QDGHCAACRAVATSSPGQRYOKGTESDPTLCONCPPGTSPN-GTLEECQHOT 183
 Db 119 KSSGCKACVSGTCKGIGYV-SGHTSAGDVICSPCGIGTYSRTVSSADKCEPVT 172

RESULT 13

057099 ID 057099 PRELIMINARY; PRT; 349 AA.

AC 057099;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRMB.
 OS Monkeypox virus.
 OC Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 CC Orthopoxvirus.
 OX NCBI_TaxID=10244;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-STERRA LEONE-1970 (70-0266);
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (Jan-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U87843; AAB94360.1; -
 DR HSSP: P25942; ICDF.
 DR INTERPRO: IPR001368; -
 DR PFAM: PF00020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SQ SEQUENCE 349 AA; 38321 MW; FE449028C933F57 CRC64;

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 25, 2001, 17:31:39 ; Search time 10.06 Seconds
(without alignments)
540.425 Million cell updates/sec

Title: US-08-741-095B-26

Perfect score: 1578
Sequence: 1 MEPPGDMGPPPMRSTPTDV.....VTVAVERTIPSTGRSPNH 283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1570	99.5	283	5	PCT-US96-12374-2
2	276.5	17.5	289	4	US-09-042-785A-11
3	267.5	17.0	277	4	US-09-042-785A-10
4	260	16.5	207	3	US-08-974-022-47
5	260	16.5	325	1	US-08-292-549-2
6	260	16.5	325	4	US-09-042-785A-9
7	260	16.5	325	4	US-09-042-785A-9
8	259	16.4	227	3	US-08-974-022-48
9	259	16.4	461	1	US-08-385-229-2
10	259	16.4	461	2	US-08-650-000-2
11	259	16.4	461	4	US-09-042-785A-7
12	259	16.4	461	6	5395760-2
13	259	16.4	461	1	US-08-243-010-1
14	259	16.4	518	1	US-08-385-229-4
15	258	16.3	197	3	US-08-974-022-49
16	257	16.3	162	2	US-08-219-237B-7
17	252	16.0	163	2	US-08-219-237B-5
18	248	15.7	164	2	US-08-332-087A-9
19	246	15.6	300	2	US-08-794-796-2
20	240.5	15.2	205	3	US-08-974-022-51
21	238.5	15.1	326	5	PCT-US91-02207-4
22	238.5	15.1	326	5	US-08-505-606-1
23	230.5	14.6	197	2	US-08-219-237B-8
24	225.5	14.3	355	1	US-08-292-549-6
25	221	14.0	139	2	US-08-219-237B-8
26	215.5	13.7	206	1	US-08-097-827-7
27	215.5	13.7	206	1	US-08-494-574-7

28	215.5	13.7	438	1	US-08-097-827-11	Sequence 11, Appl
29	215.5	13.7	438	1	US-08-494-574-11	Sequence 11, Appl
30	213.5	13.5	474	2	US-08-650-000-4	Sequence 4, Appl
31	213.5	13.5	474	4	US-09-042-785A-8	Sequence 8, Appl
32	213.5	13.5	474	6	5395760-4	Patent No. 5395760
33	210	13.3	401	3	US-08-974-022-6	Sequence 6, Appl
34	210	13.3	401	4	US-09-042-785A-12	Sequence 12, Appl
35	209.5	13.3	451	3	US-08-996-139-4	Sequence 4, Appl
36	209.5	13.3	616	3	US-08-996-139-6	Sequence 6, Appl
37	208.5	13.2	591	3	US-08-996-139-2	Sequence 2, Appl
38	206.5	13.1	417	4	US-08-815-469-4	Sequence 4, Appl
39	206.5	13.1	428	4	US-08-815-469-2	Sequence 2, Appl
40	206	13.1	335	2	US-08-219-237B-2	Sequence 2, Appl
41	206	13.1	335	2	US-08-409-338-1	Sequence 1, Appl
42	206	13.1	335	4	US-09-290-640-2	Sequence 2, Appl
43	205	13.0	335	5	PCT-US95-17083-2	Sequence 2, Appl
44	205	13.0	327	4	US-09-290-640-66	Sequence 66, Appl
45	205	13.0	605	4	US-09-042-785A-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
PCT-US96-12374-2
; Sequence 2, Application PC/TUS9612374
; GENERAL INFORMATION:
; APPLICANT: Northwestern University
; TITLE OF INVENTION: Herpes Virus Entry Mediator
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Dressler, Goldsmith, Milnamow & Katz, Ltd.
; STREET: 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12374
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Northrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: NOR3446P020PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5400
; TELEFAX: (312) 616-5460
; TELEX: --
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-12374-2

Query Match 99.5% Score 1570: DB 5: Length 283:
Best Local Similarity 99.3% Pred. No. 1.1e-133:
Matches 281: Conservative 1: Mismatches 1: Indels 0: Gaps 0:

QY 1 MEPPGDMGPPPMRSTPTDVRLVLYTFGAPCYAALPSCKDEYVSGSECCPKSPG 60
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DB 1 MEPPGDMGPPPMRSTPTDVRLVLYTFGAPCYAALPSCKDEYVSGSECCPKSPG 60
|||||
QY 61 YRKACAGELGTVCPCPGTYIAHLNGLSKLCQCDPAMGLARSRNCRTENAVCG 120
|||||

Db 61 YRVKACGELTGVCEPCPGTYIAHNGLSKLCQCMCPAMGLRATRNCSTENAVCG 120
QY 121 CSPHFCIVDDGHCACRAVATSSPGORVOKGTESDPTLCCPCPGTSPNTEECQ 180
Db 121 CSPHFCIVDDGHCACRAVATSSPGORVOKGTESDPTLCCPCPGTSPNTEECQ 180
QY 181 HQTCSWLVYKAGAGTSSSHWMMFLSGSLVIVVSTVGLITCVKRRKRGDVVKYIVS 240
Db 181 HQTCSWLVYKAGAGTSSSHWMMFLSGSLVIVVSTVGLITCVKRRKRGDVVKYIVS 240
QY 241 YVRKROEAGEATVIALQAPPDVTVAVEETIPSTGRSPNH 283
Db 241 YVRKROEAGEATVIALQAPPDVTVAVEETIPSTGRSPNH 283

RESULT 2

US-09-042-785A-11
; Sequence 11, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-042-785A-11

Query Match 17.5%; Score 276.5; DB 4; Length 289;
Best Local Similarity 27.9%; Pred. No. 1.9e-17;
Matches 69; Conservative 43; Mismatches 106; Indels 29; Gaps 8;

QY 41 SCDEEYPVSGCECPKCSPGYRVKACGELTGVCEPCPGTYIAHNGLSKLCQCMCD 100
Db 25 TCSDKOHLHDGCCDLCQPGSRILTSHCTALEKTQCHPCDSGEPSAOWNRIRCHQHRHCE 84
QY 101 PAMGLRASRNCSTENAVCGCSPGHFCIVDDGHCACRAVATSSPGORVOKGTESDPT 160
Db 85 PNGGLRKRKKGATGESPDTVYCKCKEGQHTSKD---CEACAGHTPCIRGFGVEMATETDT 141
QY 161 LCONCPGTFSPNGTL-EECGHOTKS---WLVTKAGACTSSSHWMMFLSGSLVIVV 215

Db 142 VCHPCPVGFSSNQSLFEKCYPWTSCEDKNLEVLQK---GTSQTNVYIGLKSRRALVI 198
QY 216 CSTVGLITC-----VKR--RRPRGDVAVIVSVQRRKREAGEATVIALQAPPDVT 266
Db 199 PVVAGLITTFGVFLYIKRVKKPKDN--BMLPPAARQDPQEME-----DYPGHNTA 249
QY 267 VAVEETI 273
Db 250 APVQETL 256

RESULT 3

US-09-042-785A-10
; Sequence 10, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-042-785A-10

Query Match 17.0%; Score 267.5; DB 4; Length 277;
Best Local Similarity 26.1%; Pred. No. 1.2e-16;
Matches 71; Conservative 50; Mismatches 116; Indels 35; Gaps 9;

QY 20 VLRVLVLYLFLGAPCYAPAL-----PSCKEDEVPGSECCPKCSPGYRVKACGELTGV 74
Db 1 MVRLLPQCVLMG--CLTVAHVHPRPACREKQYLLNSCCSLCQPGOKLVSCTEETETE 58
QY 75 CEPCPGTYIAHNGLSKLCQCMCPAMGLRASRNCSTENAVCGCSPGHFCIVDDGCH 134
Db 59 CLPCGSEFLDTWNRRTBHQHRYCDPNGLRVQOKGTSETPTITCEEGMHC---TSEA 115
QY 135 CAACRAVATSSPGORVOKGTESDPTLCCPCPGTSPNTEECQCHOTKCSW--LVTK 191
Db 116 CESCIVLHRCSPGFGKQATGVSPTICPCPGYGFSSNVSNAFEKCHPWTSETDLYVQ 175
QY 192 AGAGTSSSHWMMFLSGSLVIVVSTVGLITCVKRRKRGDVVKYIVSVQRRKREAGE 251

Db 176 Q-AGTNTDVCQPDRLALVPIIFGLFA-----ILLVLFYKAKKPKLNK 225

QY 252 AFVIEALQAPPDV-----TTVAVEETI 273

Db 226 AP--HPKQEPQEIINFPPDLPSNNAAPVQETL 255

RESULT 4

US-08-974-022-47

Sequence 47, Application US/08974022

Patent No. 6015938

GENERAL INFORMATION:

APPLICANT: Boyle, William J.

APPLICANT: Lacey, David L.

APPLICANT: Calzone, Frank J.

APPLICANT: Chang, Ming-Shi

TITLE OF INVENTION: OSTEOPROTEGERIN

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.

STREET: 1840 Denavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,022

FILING DATE: 12-DEC-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/577,788

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-378

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 207 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-974-022-47

Query Match 16.5%; Score 260; DB 3; Length 207;

Best Local Similarity 31.5%; Pred. No. 3.8e-16;

Matches 62; Conservative 25; Mismatches 80; Indels 30; Gaps 8;

QY 20 VLRLVLYLTLGAPCYAPALP-----SCKEDYPVGSCECCPKSPGYRVKACGELTGT 73

Db 1 MLRLIALLCV-VVYGDVDPYSSNCGKHDEKDLCCASHCPFYASRLCGPSNT 59

QY 74 VCEPCPGTYIAHNGSKLCQCMCPAMG-LRASRNCSTENAVCGSGPHFCIVODG 132

Db 60 VCSPEDEGTFTASTNHAAPACVSCR--GPGTGHLESOPCDTHRVNCSTGNCLKGQ 117

QY 133 DHCACRAVYATSSPGQVQKGTESODTLCONCPGTFSPN-GTLEEC----- 179

Db 118 NGCIGIC-APQTKCPAGVSGHTRAGDTLCEKCPHTYSLSLSTFKCGTSFNYSVGFN 176

QY 180 ---OHQTKCSMLVTKAG 193

Db 177 LYPVNETSCT---TTAG 190

RESULT 5

US-08-292-549-2

Sequence 2, Application US/08292549

Patent No. 5464938

GENERAL INFORMATION:

APPLICANT: Smith, Craig A.

APPLICANT: Goodwin, Raymond G.

TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/292,549

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/963,330

FILING DATE: 10/19/92

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2602-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 325 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-292-549-2

Query Match 16.5%; Score 260; DB 1; Length 325;

Best Local Similarity 31.5%; Pred. No. 6.6e-16;

Matches 62; Conservative 25; Mismatches 80; Indels 30; Gaps 8;

QY 20 VLRLVLYLTLGAPCYAPALP-----SCKEDYPVGSCECCPKSPGYRVKACGELTGT 73

Db 1 MLRLIALLCV-VVYGDVDPYSSNCGKHDEKDLCCASHCPFYASRLCGPSNT 59

QY 74 VCEPCPGTYIAHNGSKLCQCMCPAMG-LRASRNCSTENAVCGSGPHFCIVODG 132

Db 60 VCSPEDEGTFTASTNHAAPACVSCR--GPGTGHLESOPCDTHRVNCSTGNCLKGQ 117

QY 133 DHCACRAVYATSSPGQVQKGTESODTLCONCPGTFSPN-GTLEEC----- 179

Db 118 NGCIGIC-APQTKCPAGVSGHTRAGDTLCEKCPHTYSLSLSTFKCGTSFNYSVGFN 176

QY 180 ---OHQTKCSMLVTKAG 193

Db 177 LYPVNETSCT---TTAG 190

RESULT 6

US-09-042-785A-9

Sequence 9, Application US/09042785A

Patent No. 6194151

GENERAL INFORMATION:

APPLICANT: Busfield, Samantha J

TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
City: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-042-785A-9

Query Match 16.5%; Score 260; DB 4; Length 325;
Best local Similarity 31.5%; Pred. No. 6.6e-16;
Matches 62; Conservative 25; Mismatches 80; Indels 30; Gaps 8;

QY 20 VLRLVLTFLGACVAPALP-----SKDEYPVSECCPSGKYRKVACGELTGT 73
DB 1 MLRLIALVCV-VVYGDVDPYSSNCGKHDEKDLCCASCHPGFYASRLCGPSNT 59
QY 74 VCEPCPGTYIAHLNGLSKLCQCMCDPAMG-LRASRCSRTENAVCGSPGHFCIYODG 132
DB 60 VCSPEDEGFTASTNNHAPACVSCR--GPCGHLSESGPCDRTHRVNCSTGNVCLLKQ 117
QY 133 DHCACRAVATSSPGQYOKGTESDTLQNCPPGTFSFN-GTLEEC-----179
DB 118 NGCRIC-APQTKCPAGYGVSGHTRAGDTLCEKCPHTYSDSLSPTEKGTSTFNYSVGFN 176
QY 180 ---QHOKCSMLVTKAG 193
DB 177 LYPVNETSCT---TTAG 190

RESULT 7
PCT-US91-02207-2
Sequence 2, Application PC/TUS9102207
GENERAL INFORMATION:
APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Isolated Viral Protein Cytokine Antagonists
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
City: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02207
FILING DATE: 19910329
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wright, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2602
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 587-0606
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-02207-2

Query Match 16.5%; Score 260; DB 5; Length 325;
Best local Similarity 31.5%; Pred. No. 6.6e-16;
Matches 62; Conservative 25; Mismatches 80; Indels 30; Gaps 8;

QY 20 VLRLVLTFLGACVAPALP-----SKDEYPVSECCPSGKYRKVACGELTGT 73
DB 1 MLRLIALVCV-VVYGDVDPYSSNCGKHDEKDLCCASCHPGFYASRLCGPSNT 59
QY 74 VCEPCPGTYIAHLNGLSKLCQCMCDPAMG-LRASRCSRTENAVCGSPGHFCIYODG 132
DB 60 VCSPEDEGFTASTNNHAPACVSCR--GPCGHLSESGPCDRTHRVNCSTGNVCLLKQ 117
QY 133 DHCACRAVATSSPGQYOKGTESDTLQNCPPGTFSFN-GTLEEC-----179
DB 118 NGCRIC-APQTKCPAGYGVSGHTRAGDTLCEKCPHTYSDSLSPTEKGTSTFNYSVGFN 176
QY 180 ---QHOKCSMLVTKAG 193
DB 177 LYPVNETSCT---TTAG 190

RESULT 8
US-08-974-022-48
Sequence 48, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavenland Drive
City: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:

RESULT 14
 US-08-385-229-4
 : Sequence 4, Application US/08385229
 Patent No. 5605690
 GENERAL INFORMATION:
 APPLICANT: Jacobs, Cindy A.
 APPLICANT: Smith, Craig A.
 TITLE OF INVENTION: Method of Treating TNF-Dependent
 TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: Washington
 COUNTRY: U.S.A.
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/385,229
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/946,236
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Wight, Christopher L.

OY	35	YAPLPLP-CKEDDEV- -PVGSECCRCGSGYHVKACCEILGTGVEPCPPCTYYIAHLNGLS	91
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	61	YAPGPGSTCRREYYDGTQAMCCSKCGSGQHAKEVCTKPSDTVDCGSDSTYYQLMMWVP	120
OY	92	KCLQCCQMDPAMGLRASNN-----GSTRTEAVGCGSPGHCTIQQDDDHCAACAAVATSS	145
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	121	ECLSC-----GSRCSDDYETQACTREQRNRTICTCRPMWICALSKQEGCHLCAPLAKCR	173
OY	146	PGQRYQKGGTSSQTLQCNCPPTGFS- -PNGTLECCQHQTKCSMLVTKAGAG-----TSSS	199
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	174	PGFGVARGTGTSDVCKPCCAGFTFSNTSTDICRPHQIQCNVVALPGNNSMDAVCTST	233

```

15 RESULT
16 US-08-974-022-49
17 Sequence 49, Application US/08974022
18 Patent No. 6015938
19 GENERAL INFORMATION:
20 APPLICANT: Boyle, William J.
21 APPLICANT: Lacey, David L.
22 APPLICANT: Calcione, Frank J.
23 APPLICANT: Chang, Ming-Shi
24 TITLE OF INVENTION: OSTEOPROTEGERIN
25 NUMBER OF SEQUENCES: 53
26 CORRESPONDENCE ADDRESSES:
27 ADDRESSEE: Amgen Inc.
28 STREET: 1840 Dehavenland Drive
29 CITY: Thousand Oaks
30 STATE: California
31 COUNTRY: USA
32 ZIP: 91320-1789
33 COMPUTER READABLE FORM:
34 MEDIUM TYPE: Floppy disk
35 COMPUTER: IBM PC compatible
36 OPERATING SYSTEM: PC-DOS/MS-DOS
37 SOFTWARE: PatentIn Release #1.0, Version #1.30
38 CURRENT APPLICATION DATA:
39 APPLICATION NUMBER: US/08/974,022
40 FILING DATE: 12-DEC-1995
41 CLASSIFICATION:
42 PRIOR APPLICATION DATA:
43 APPLICATION NUMBER: 08/577,788
44 FILING DATE:
45 ATTORNEY/AGENT INFORMATION:
46 NAME: Wintler, Robert B.
47 REFERENCE/DOCKET NUMBER: A-378
48 INFORMATION FOR SEQ ID NO: 49:
49 SEQUENCE CHARACTERISTICS:
50 LENGTH: 197 amino acids
51 TYPE: amino acid
52 STRANDEDNESS: single
53 TOPOLOGY: linear
54 MOLECULE TYPE: protein
55 US-08-974-022-49

```


Db 199 PVMGILITIFGVFLYIKKVKKKPKDN--EMLPPAARRQDPQENE-----DYPGNHTA 249
 QY 267 VAVEETI 273
 Db 250 APVOETL 256

RESULT 2

A60771
 B-cell activation protein CD40 precursor - human
 N:Alternate names: B-cell surface antigen Bp50
 C:Species: Homo sapiens (man)
 C>Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
 C:Accession: S04460; A60771
 R:Stamenkovic, I.; Clark, F.A.; Seed, B.
 EMBL J. 8, 1403-1410, 1989
 A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
 A:Reference number: S04460; MUID:89356608
 A:Accession: S04460
 A:Molecule type: mRNA
 A:Residues: 1-277 <STA>
 A:Cross-references: EMBL:X05092; NID:929850; PIDN:CAA3045.1; PID:929851
 R:Brasch, Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
 J. Immunol. 142, 562-567, 1989
 A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-Lik
 A:Reference number: A60771; MUID:89093941
 A:Accession: A60771
 A:Molecule type: protein
 A:Residues: 21-50 <BRA>
 A:Experimental source: Burkitt lymphoma cell line Raj1
 C:Genetics:
 A:Gene: GDB:CD40
 A:Cross-references: GDB:215268; OMIM:109535
 A:Map position: 20q12-20q13.2
 C:Superfamily: CD27 antigen; NGF receptor repeat homology
 C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
 F:21-193/Domain: extracellular #status predicted <EXT>
 F:194-215/Domain: transmembrane #status predicted <TM>
 F:216-277/Domain: intracellular #status predicted <CYT>
 F:153/180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.0%; Score 267.5; DB 2; Length 277;
 Best Local Similarity 26.1%; Pred. No. 1.1e-12;
 Matches 71; Conservative 50; Mismatches 116; Indels 35; Gaps 9;

QY 20 VLRLVLYLFLGAPCYAPAL-----PSCKEDYPVSECCPKSPGYRVKREACGELTGV 74
 Db 1 MVRRLPLOCVLWG--CLITAVHPRPTACRKKQYLINQCCSLCPGKGLVSDCFEETETE 58
 QY 75 CEECPPTGYIAHLNGLSKLQCCOMCDPAMG-LRASRNCSTENAVCGSPGHFCTIVODG 134
 Db 59 CLPCESEFLDPTWNRHETHQHKKYCDNLGLRVQCKTSEDTICTCEEGWHC---TSEA 115
 QY 135 CACRAATATSPGQRYVKGKTESODTLCQNCPRPTFS-PKCTLECHQHOKCSM--LYTK 191
 Db 116 CESCVLHRSCTPGFVQKATGVSDTICEPCVGFNSVSAPEKCHPMTSCETKRDLYVQ 175
 QY 192 AGATSSSHWMEFLSGSLYIVICSTVGLICVRRKPRGDDVYKIVSVQKROAEAGE 251
 Db 176 Q-AGTNKTDVYVCGPQDRLRALVYPIITFGILFA-----ILLVVFYIKKVAKKPTNK 225
 QY 252 ATVTEALQAPPDV-----TTVAVEETI 273
 Db 226 AP--HPKQEPQEIFPDDLPGSNTAAVQETL 255

RESULT 3
 B43692
 T2 protein - rabbit fibroma virus

C:Species: rabbit fibroma virus, Shope fibroma virus
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: B43692
 R:Upton, C.; Delange, A.M.; McFadden, G.
 Virology 160, 20-30, 1987
 A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomer
 A:Reference number: A43692; MUID:87321103
 A:Accession: B43692
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-325 <OPT>
 A:Cross-references: GB:M17433
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
 F:64-105/Domain: NGF receptor repeat homology <NG>
 F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 16.5%; Score 260; DB 2; Length 325;
 Best Local Similarity 31.5%; Pred. No. 4.3e-12;
 Matches 62; Conservative 25; Mismatches 80; Indels 30; Gaps 8;

QY 20 VLRLVLYLFLGAPCYAPAL-----SCKEDYPVSECCPKSPGYRVKREACGELTGV 73
 Db 1 MLRLIALVCV-VVYGDVDPYSSNCGKCGHDEKDLGCASCCHPFGYASRLCGPSNT 59
 QY 74 VCECPPTGYIAHLNGLSKLQCCOMCDPAMG-LRASRNCSTENAVCGSPGHFCTIVODG 132
 Db 60 VCSPECEGTFTTASTINAPACVSCR--GPTGHLSESPCPRCTRDRVCNCTGNYCLLKG 117
 QY 133 DHCACRAVATSSPGQRYVKGKTESODTLCQNCPRPTFSN-GLTEBC----- 179
 Db 118 NCGRIC-APQTKCPAGVSGVGHTRAGDTLCEKPPHTYSLSLPTERCGRSFNVISGFN 176
 QY 180 ---OHQTKCSMLYTKAG 193
 Db 177 LYPVENISCT--TTAG 190

RESULT 4

A35356
 Tumor necrosis factor receptor 2 precursor [validated] - human
 N:Alternate names: 75k tumor necrosis factor receptor; TNF receptor type 2
 C:Species: Homo sapiens (man)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
 C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; J18094
 R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990
 A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular
 A:Reference number: A35356; MUID:90260639
 A:Accession: A35356
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-461 <SM1>
 A:Cross-references: GB:M32315; NID:9189185; PIDN:AAA59929.1; PID:9189186
 R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squit Pro. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
 A:Title: A second tumor necrosis factor receptor gene product can shed a naturally oc
 A:Reference number: A36475; MUID:91045991
 A:Accession: A36475
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-195; R' 197-461 <KOH>
 A:Cross-references: GB:M55594; GB:M38549; NID:9339757; PIDN:AAA36755.1; PID:9339758
 R:Dembluc, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lamm, H.W.; Gentz, R.; Brockhaus, Cytokine 2, 231-237, 1990
 A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular
 A:Reference number: A48416; MUID:91370690
 A:Accession: A48416
 A>Status: preliminary
 A:Molecule type: mRNA; protein
 A:Residues: 23-461 <DEM>
 A:Cross-references: GB:S63368; NID:9235648; PIDN:AA19824.1; PID:9235649
 A>Note: sequence extracted from NCBI backbone (NCBI:63368, NCBI:63371)

QY 178 ECQ-----HQTCSMLVTKAGAGTSSSHWMMFLSGSLVIYI 214
 Db 178 YIDVEITLVPVNDPSCRTT---TGLSES-----ILTSLITIM 214

RESULT 7

gene GAR protein - variola virus
 N:Alternate names: B28R protein (COP)
 C:Species: variola virus
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Oct-1999
 C:Accession: D36858; S46888; S32385; S35987
 R:Blinov, V.M.
 Submitted to Genbank, November 1992
 A:Description: not shown.
 A:Reference number: A36859
 A:Accession: D36858
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-349 <BLI>
 A:Cross-references: GB:X69198; NID:9456758; PIDN:CAA49137.1; PID:9457087
 A:Experimental source: strain India-1967, ssp. major, isolate Ind3
 R:Kolymhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Etol
 Submitted to the EMBL Data Library, April 1992
 A:Description: Nucleotide sequence analysis of the region of variola virus XhoI F O H P
 A:Reference number: S46868
 A:Accession: S46888
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-349 <KOL>
 A:Cross-references: EMBL:X67117; NID:9516428; PIDN:CAA47540.1; PID:9516449
 A:Experimental source: strain India-1967, isolate Ind3
 R:Shchelnikov, S.N.; Blinov, V.M.; Sandakchiev, L.S.
 FEBS Lett. 319, 80-83, 1993
 A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
 A:Reference number: S32385; MUID:93202281
 A:Accession: S32385
 A:Molecule type: DNA
 A:Residues: 31-168 <SHC>
 A:Cross-references: EMBL:X69198
 A:Experimental source: strain India-1967, ssp. major
 C:Genetics: GAR
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
 F:32-66/Domain: NGF receptor repeat homology <NGF>
 F:68-109/Domain: NGF receptor repeat homology <NG2>
 F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 16.3%; Score 257; DB 2; Length 349;
 Best Local Similarity 29.3%; Pred. No. 7, 6e-12;
 Matches 66; Conservative 23; Mismatches 94; Indels 42; Gaps 8;
 QY 21 LRLVLYTLFGAPC-----YADALPSCKEDEVPSGCCPKSPGYRVEACGEL 70
 Db 1 MKSIVLYIIFLSCIIINGRDAAPYTPNGCKCKDEYKRNNLCLSCPPGTASRLCDK 60
 QY 71 TGVYCECPPTGYTAHNLGSKLCQO-MCDPAMGLASRNCSTENAVAGCGSGHICIV 129
 Db 61 TMTQCPGCGGTFTSRNNHLPACLSGCRGN--SNQVETSCMTHNRICEGSGYYCCL 118
 QY 130 ODGDHCAACAVYATSSGQGVOKGKTSDTLCONCPGPFSS-----PNCGLE 177
 Db 119 KGSSGCAACVSQTKCGIGYV-SGHTSVGVIVICSPCGFGYSHTVSSADKCEPVNNTFN 177
 QY 178 ECQ-----HQTCSMLVTKAGAGTSSSHWMMFLSGSLVIYI 214
 Db 178 YIDVEITLVPVNDPSCRTT---TGLSES-----ILTSLITIM 214

RESULT 8

tumor necrosis factor receptor 2-related protein - human
 C:Species: Homo sapiens (man)
 C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
 C:Accession: I54182
 R:Beens, M.; Chalfant, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
 Genomics 16, 214-218, 1993
 A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq
 A:Reference number: I54182; MUID:93252381
 A:Accession: I54182
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-435 <RES>
 A:Cross-references: GB:L04270; NID:9339761; PIDN:AAA36757.1; PID:9339762
 C:Genetics: LTR
 A:Cross-references: GDB:1230195; OMIM:600979
 A:Map position: 12p13.3-12p13.1
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 16.0%; Score 253; DB 2; Length 435;
 Best Local Similarity 26.7%; Pred. No. 1, 8e-11;
 Matches 86; Conservative 37; Mismatches 127; Indels 72; Gaps 16;
 QY 4 PG-DWGPMPRSTPRDVLRLVLYTLFL-----GAPCYAPALPSCK--EDXY--PVGS 51
 Db 10 PGLAMGP-----LVGLGFLAASQPQAVPYASBNQCRDQEKREYEPQHR 56
 QY 52 ECPKSPGTRVKEAGELGTVCCEPPGTIYAHNLGSKLCQOCMPAMGLASRNC 111
 Db 57 ICSSRCPPGTGYVAKSCSRIDTCATCAENSYNEMHWYLTICOLCRCPDVMGLEIAPC 116
 QY 112 SREINAVCGSGPHFCIVQDGDHCACRAVATSSPG-----ORVKGTESDTLCONC 165
 Db 117 TSKRTQCRQRPMEFCAM-ALECHTELLSDCPGTEALKEBVGKNNH-----CVIC 170
 QY 166 PGTFF--SPNCTLEECQHQTKC-SMLVTKAGAGTSSSHWMM-----FLSGSLVI 212
 Db 171 KAGHQTSSPSA---RCQPHTCENGLVEAPAGTAQSDPTCKNPLELPMSGTMLM 227
 QY 213 VIVCSYVGLI-----CYKRRKPRGDVYKIVSVQKQKEAGEYIEALQAP----- 261
 Db 228 LAVLLPLAFLLATVFSCTIKWSHP--SLCKRLGSLILKRRPDQEGPNVAGSWEPKAP 285
 QY 262 --PDVTTVAVEETIPSPFTGRSP 281
 Db 286 YFPDL-----VQPLPIPSGDVSP 303

RESULT 9

S12783
 OX40 antigen precursor - rat
 N:Alternate names: nerve growth factor receptor homology
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
 C:Accession: S12783; S08036
 R:Maliet, S.; Fossum, S.; Barclay, A.N.
 EMBO J. 9, 1063-1068, 1990
 A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphoc
 A:Reference number: S12783; MUID:90214614
 A:Accession: S12783
 A:Molecule type: mRNA
 A:Residues: 1-271 <MAI>
 A:Cross-references: EMBL:M17037; NID:957830; PIDN:CAA34897.1; PID:957831
 C:Superfamily: CD27 antigen; NGF receptor repeat homology
 C:Keywords: growth factor receptor; transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-271/Product: OX40 antigen #status predicted <MAT>
 F:211-235/Domain: transmembrane #status predicted <TM>

Query Match 15.2%; Score 240.5; DB 2; Length 271;
 Best Local Similarity 34.9%; Pred. No. 9, 9e-11;

[illegible]

RESULT 10
GOVZML
T2 protein - myxoma virus (strain Lausanne)
C:Species: myxoma virus
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C:Accession: A40566
R:Upton, C.; Macen, J.L.; Schreiber, M.; McFadden, G.
Virology 184, 370-382, 1991
A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis
A:Reference number: A40566, MUID:91335768
A:Accession: A40566
A:Molecule type: DNA
A:Residues: 1-326 <DPT>
A:Cross-references: GB:995181; GB:M37976; NID:g332309; PIDN:AAAA6632.1; PID:g332310
C:Superfamily: myxoma virus T2 protein; NCF receptor repeat homology
C:Keywords: glycoprotein
E:64-105/Domain: NCF receptor repeat homology <NG3>
E:106-147/Domain: NCF receptor repeat homology <NG3>
E:66,181,205,238/Binding site: carbonyl site (Asn) (covalent) #status predicted

Query Match	15.1%	Score 238.5	DB 1	Length 326
Best Local Similarity	26.8%	Pred. No. 1.6e-10		
Matches 73, Conservative	30	Mismatches 104	Indels 65	Gaps 11

```

QY      20  VLRIVLVLTPL-----GACVYAPALPSCSEDEYAPVSGECCPSCPYRYKAEKAGELTGT 73
      1  MFRLLTLLAVAYACVYGGAP--YGADRGCKCRGNDEYKDKGLCTSCPPSYASRLCGPESDI 59
QY      74  VCECECPPGCTYAHNLNGSLCKLQCG--MDDPAMGLBARSNCERTENAVCGCGPHFCLYQDG 132
      60  VCSCCKMETFTASTNHAAPACVSCGCRG--TGHLSSESSCKDTRDYDDCSAGNYCYLLKG 117
QY      133  DHCACACRAYATTSFGQVROKGGTGESDPTLONCPGTFSPN--GTMLECQ-----180
      118  EGCICIC-APKTKPCAGVGSGHRTGTYGLCTKCPRTYISDAVSTETCTISFPNISEFN 176
QY      181  ---HQTCKSLVYKAGA-----GTSSHWMMWFLSGS 209
Db      177  LYPVNDTSC---TTAGPNEVYKTSSESVTLNHTDCDPVEHTEYEGTSGSEGAGGFTGM 233
QY      210  ---LVIVYCSVGLLIIIVKRRKRGDGVVVI 238
Db      234  DRYONTTKMCLNIEIKCIV-----GVAVRTI 260

```

RESULT 11
148700
gene ox40 protein - mouse
N:Alternate names: ox40 antigen
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence,revision 02-Jul-1996 #text,change 11-Jan-2000
C:Accession: 148700; 148334; S34377
J:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
J. Immunol. 151, 5261-5271, 1993
A:Title: Cloning of mouse Ox40, a T cell activation marker that may mediate T-B cell int
A:Reference number: 148700; MUID:94044750
A:Accession: 148700

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-272 <RES>
A:Cross-references: EMBL:Z21674; NID:9312827; PIDD:CAA79772.1; PID:9312828
R:Birkeland, M.L., Copeland, N.G., Gilbert, D.J., Jenkins, N.A., Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX
A:Reference number: I48334; MUID:95255413
A:Accession: I48334
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-14, G', 16-272 <RE2>
A:Cross-references: EMBL:X85214; NID:9732818; PIDD:CAA59476.1; PID:9732819
C:Genetics:
A:Gene: ox40
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C:Superfamily: CD27 antigen; NCF receptor repeat homology

	Query Match	13.7%;	Score 215.5;	DB 2;	Length 272;
	Best Local Similarity	31.5%;	Pred. 6.7e-09;		
	Matches 46;	Conservative 17;	Mismatches 58;	Indels 25;	Gaps
Oy	41	SCKEDYEVSGECSPKPSGYRYKEAGSELGTVCCEPCRPSTYTALHNGLSKLQCCMCD	100		
	:	: : : : : : :	: : :		
Db	26	NCVHTTYSGHKCCRCRCPGHWSRDHDFTDLCHPCEGFYEAVN-YDTCKQTQCIN	84		
Oy	101	FAMGLRASRNCSRTLENAYCGSSPFHFCLVDGDHCACRAATNSSPGQRVQKGTSQDT	160		
	:	: : : : : : :	: : :		
Db	85	HRSSEGLKQNTPTPDYVCRRCRPG-----TQP--RDSDGKLGVD-	122		
Oy	161	LCONCPGTFSPNGTLRECOHQTKCS	186		
	:	: : : : :			
Db	123	-CVPRPPGHFSP-GNNQACKPWITCT	146		

RESULT 12

B38634

tumor necrosis factor receptor type 2 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999

C:Accession: B38634; A40254; S54816

R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factors

A:Reference number: A38634; MUID:q1187885

A:Accession: B38634

A:Molecule type: mRNA

A:Residues: 1-474 <LEM>

A:Cross-references: GB:560469; NID:g199827; PIDN:AAA3752.1; PID:g199828

R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J Mol. Cell. Biol. 11, 3020-3026, 1991

A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f

A:Reference number: A40254; MUID:q1246168

A:Accession: A40254

A:Molecule type: mRNA

A:Residues: 1-474 <GOO>

A:Cross-references: GB:560469; NID:g199827; PIDN:AAA3752.1; PID:g199828

R:Kismonerhis, M.; Felloows, R.; Feldmann, M.; Chernafovsky, Y. submitted to the EMBL Data Library, May 1995

A:Description: Characterization of the promoter region of the murine p75-TNF receptor

A:Reference number: S54816

A:Accession: S54816

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-22 <KIS>

A:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044

C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homolog

C:Keywords: cytokine receptor; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <IG>

F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MT>

F:40-77/Domain: NGF receptor repeat homology <NG1>

F:79-120/Domain: NGF receptor repeat homology <NG2>

A:Note: In NCBI backbone the source is designated as mouse
C:Genetics:

A:Gene: GDB:APT1

A:Cross-references: GDB:132671; OMIM:134637

A:Map position: 10q24.1-10q24.1

C:Superfamily: NGF receptor repeat homology

C:Keywords: apoptosis; surface antigen; transmembrane protein

F:1.16/Domain: signal sequence #status predicted <SIG>

F:85-128/Domain: NGF receptor repeat homology <NG4>

F:174-190/Domain: transmembrane #status predicted <TM>

Query Match 13.1%; Score 206; DB 2; Length 335;
Best Local Similarity 25.0%; Pred. No. 3.9e-08;

Matches 60; Conservative 30; Mismatches 82; Indels 68; Gaps 9;

```
QY 50 GSECCPKCSFGYRKKEACGELTGV-----CEPCPPG---TYIAHLNGLSKLQCOMCD 100
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 56 GQFCCHKPCPPGERKARDC-----TVNGDEPDVCVPCQEGKEYTDKAHFS--SKCRRCRLCD 108
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 101 PAMGLRASRNCSTENAVCGSPGHFCIVQDDGHCAACRAVATSSPGQRYQKGSTESQDT 160
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 109 EGHGLEVEINCTRTQNTKCKCKPFFC-----NST 138
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 161 LCQNCPPGTSPNGTLEEC--OHQTKCSMLVTRAGAGTSSSHWVWVFLSGSLVIYIVCST 218
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 139 VCEHCDPCTCEHGIKECTLTSTKTC-----KEGSRSNLGM-----LCILLLP 183
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 219 VGLICVKKRRKPRGDVYKIVSVQRRKQEAEGEATVIEALQAPPDVTVAVEETIPSFTEG 278
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 184 IPLIVWVKRE-----VQKTCRKRHKREMGSHSPTLNPETVAINLSDVDLSKYITTTIAG 238
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Search completed: April 25, 2001, 17:34:47
Job time: 188 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2001, 17:34:34 ; Search time 8.99 Seconds

(without alignments)
1078.343 Million cell updates/sec

Title: US-08-741-095b-26

Percent score: 1578
1 MEPPGDMGPPMRSTPRTDV.....VTVAVETIPSTGRSPNH 283

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	276.5	17.5	289	CD40_MOUSE	P27512 mus musculus
2	267.5	17.0	277	CD40_HUMAN	P25942 homo sapien
3	267	16.9	269	CD40_BOVIN	Q28203 bos taurus
4	260	16.5	325	VT2_SEVKA	P25943 shope fibro
5	259	16.4	461	TNR2_HUMAN	P20333 homo sapien
6	257	16.3	349	WC22_VARY	P4015 variola vir
7	253	16.0	435	TNR2_HUMAN	P36941 homo sapien
8	245.5	15.6	415	TNR2_MOUSE	P30284 mus musculus
9	240.5	15.2	271	OX40_RAT	P15725 rattus norv
10	238.5	15.1	326	VT2_MYXVL	P29825 myxoma viru
11	236	15.0	332	FASA_PIG	077736 sus scrofa
12	215.5	13.7	272	OX40_MOUSE	P47741 mus musculus
13	213.5	13.5	474	TNR2_MOUSE	P25119 mus musculus
14	206.5	13.1	324	FASA_RAT	Q63199 rattus norv
15	206.5	13.1	417	WSL1_HUMAN	Q93038 h wsl-1 pro
16	206	13.1	335	FASA_HUMAN	P25445 homo sapien
17	205	13.0	327	FASA_MOUSE	P25446 mus musculus
18	203.5	12.9	425	NGFR_RAT	P07174 rattus norv
19	200.5	12.7	323	FASA_BOVIN	P1867 bos taurus
20	198.5	12.6	416	NGFR_CHICK	P18519 gallus gall
21	194.5	12.3	277	OX40_HUMAN	P3469 homo sapien
22	192	12.2	461	TNR1_RAT	P22934 rattus norv
23	190	12.0	427	NGFR_HUMAN	P08134 homo sapien
24	176.5	11.2	256	ALBB_MOUSE	P20334 mus musculus
25	172.5	10.9	461	TNR1_PIG	P05355 sus scrofa
26	171.5	10.9	471	TNR1_BOVIN	O19131 bos taurus
27	171	10.8	250	CD27_MOUSE	P41272 mus musculus
28	168.5	10.7	454	TNR1_MOUSE	P25118 mus musculus
29	161	10.2	255	ALBB_HUMAN	O07011 homo sapien
30	159	10.1	595	CD30_HUMAN	P28908 homo sapien
31	155	9.8	455	TNR1_HUMAN	P19438 homo sapien
32	148	9.4	260	CD27_HUMAN	P26842 homo sapien
33	143.5	9.1	1786	LMB1_HUMAN	P07942 homo sapien

34	133.5	8.5	4393	1	PGBM_HUMAN	P98160 homo sapien
35	130.5	8.3	1786	1	LMB1_MOUSE	P02469 mus musculus
36	127.5	8.1	3707	1	PGBM_MOUSE	P05793 mus musculus
37	126	8.0	1557	1	LM1L_CAEL	O18823 caenorhabdi
38	126	8.0	1798	1	LMB2_HUMAN	P55268 homo sapien
39	125	7.9	722	1	DL1L_MOUSE	Q61483 mus musculus
40	122	7.7	714	1	DL1L_RAT	P76777 rattus norv
41	122	7.7	3106	1	LM2A_MOUSE	Q60675 mus musculus
42	121.5	7.7	1964	1	NTCA_MOUSE	P31695 mus musculus
43	121	7.7	755	1	COMP_RAT	P35444 rattus norv
44	120.5	7.6	1799	1	LMB2_MOUSE	O61292 mus musculus
45	118	7.5	1696	1	PCK5_BRACL	Q9nj15 branchiosto

ALIGNMENTS

```

RESULT 1
CD40_MOUSE STANDARD; PRT; 289 AA.
ID CD40_MOUSE
AC P27512;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
GN TNFRSF5 OR CD40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92105763; PubMed=1370315;
RA Torres R.M., Clark E.A.;
RT "Differential increase of an alternatively polyadenylated mRNA
RT species of murine CD40 upon B lymphocyte activation.";
RL J. Immunol. 148:620-626(1992).
RN [2]
RP REVISIONS.
RC STRAIN=BA1B/C;
RA Torres R.M.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C; TISSUE=Liver;
RX MEDLINE=93094586; PubMed=1281194;
RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
RA Howard M., Cockayne D.A.;
RT "Genomic structure and chromosomal mapping of the murine CD40 gene.";
RL J. Immunol. 149:3921-3926(1992).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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CC
DR EMBL; M83312; AAB08705.1; -
DR EMBL; M94126; AAA37404.1; -
DR EMBL; M94129; AAA37404.1; JOINED.
DR EMBL; M94128; AAA37404.1; JOINED.
DR EMBL; M94127; AAA37404.1; JOINED.
DR PIR; A46476; A46476.
DR HSSP; P25942; 1CDF.
DR MGD; MGI:88336; Tnftrsf5.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.

```

DR	PROSITE: PS50050; TNFR,NGFR.2; 4.
KM	Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT	SIGNAL 1 19
FT	CHAIN 20 289
FT	DOMAIN 20 193
FT	TRANSMEM 194 215
FT	DOMAIN 216 289
FT	DOMAIN 215 187
FT	REPEAT 25 60
FT	REPEAT 61 103
FT	REPEAT 104 144
FT	REPEAT 145 187
FT	CARBOHYD 153 153
SO	SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;

Query Match	17.5%;	Score 276.5;	DB 1;	Length 289;
Best Local Similarity	27.9%;	Pred. No. 1.4e-15;		
Matches 69;	Conservative 43;	Mismatches 106;	Indels 29;	Gaps 8

QY	41	SCKEDEYVSECCPKSPGRVAKVACGELGTWCCEPPEPTYIAHJNGSLKOCOMCD	100
Db	25	TCSKDQYIHDQCCDCLCPGSRILSHKTALEKTCCHPCDSEFSAOMNREIJCQHNHCE	84
QY	101	PAMGLRASRNCSTREMAVCGCSPGHFCITVDDGDHCAACRAVATSSPGORVQKGTESODT	160
Db	85	PNQGRVAKVEKSTAESDFVCEKCEGQHCYSKD---CEACQAHPTCIPGFGVEMATEETDT	144
QY	161	LCQNCPESTPEPNCTL--EECHQHKCS---WLVTKAGAGTSSSHVWWFLSGSLVIV	215
Db	142	VCHRCPPGVGFSSNOSLSEKCTPMVTSCEDKNLEVLQK---GTSQTNVTCGLKSRMRALLVI	198
QY	216	CSYGLIILC-----VKR--RKPRGDVVKVIVSVQRRQEAEGEATVIALQAPPDVT	266
Db	199	PVMVGILITIGFVLYIKKKVKKPKDN--EMLPAAARRQDPQEME-----DYPGHNTA	249
QY	267	VAVEETI 273	
Db	250	APVOETL 256	

RESULT	2
CD40_HUMAN	
ID	CD40_HUMAN
STANDARD;	PRT;
277	AA.
AC	P25942;
DT	01-MAY-1992 (Rel. 22, Created)
DT	01-MAY-1992 (Rel. 22, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)
DE	(TUMOR NECROSIS FACTOR RECEPTOR 5).
GN	TNFRSF5 OR CD40.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RA	[1]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=69356608; Pubmed=2475341;
RA	Stamenkovic I., Clark E.A., Seed B.;
RT	"A B-lymphocyte activation molecule related to the nerve growth
RT	factor receptor and induced by cytokines in carcinomas.";
RL	EMBO J. 8:1403-1410(1989).
RL	[2]
RP	3D-STRUCTURE MODELING OF 24-144.
RP	MEDLINE=97189482; Pubmed=9037712;
RA	Bajorath J., Aruffo A.;
RT	"Construction and analysis of a detailed three-dimensional model of
RT	the ligand binding domain of the human B cell receptor Cd40.";
RL	Proteins 27:59-70(1997).
RL	[3]
RP	3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RP	MEDLINE=98266353; Pubmed=9605317;
RA	Slough J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,

RA zhenq 2 NatSmith J.H., Thomas P;
RT "the role of polar interactions in the molecular recognition of CD40L
RT with its receptor CD40.";
RL Protein Sci. 7:1124-1135(1998).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC -1- SIMILARITY: CONTAINS A LA-NGER/INFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
CC -----
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CC or send an email to license@isb-sib.ch).

DR	EMBL; X60592; CA43045.1; -.		
DR	PIR; S04460; S04460.		
DR	PDB; 1CDF; 01-APR-97.		
DR	MIM; 109535; -.		
DR	InterPro: IPR001368; -		
DR	Pfam; PF00020; TNFR_C6; 4.		
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.		
DR	PROSITE; PS50050; TNFR_NGFR_2; 4.		
KW	Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;		
KW	3D-structure.		
FT	SIGNAL	1	19
FT	CHAIN	20	277
FT	DOMAIN	20	193
FT	TRANSMEM	194	215
FT	DOMAIN	216	277
FT	DOMAIN	25	187
FT	REPEAT	25	60
FT	REPEAT	61	103
FT	REPEAT	104	144
FT	REPEAT	145	187
FT	DISULEID	26	37
FT	DISULEID	38	51
FT	DISULEID	41	59
FT	DISULEID	62	77
FT	DISULEID	83	103
FT	DISULEID	105	119
FT	DISULEID	111	116
FT	DISULEID	125	143
FT	CARBOYD	153	153
FT	CARBOYD	180	180
FT	SEQUENCE	277 AA;	30619 MW;
			N-LINKED (GLCNAC. . .) (POTENTIAL).
			N-LINKED (GLCNAC. . .) (POTENTIAL).
			BC08776EC2CA45680 CRC64;

Query Match	17.0%	Score	267.5	DB. 1	Length	277;	
Best Local Similarity	26.1%	Pred. No.	7.2e-15;				
Matches 71; Conservative	50;	Mismatches	116;	Indels	35;	Gaps	9;

[illegible]

Db 226 AP--HPKQFQEIHPDDLPESNTAPVQETL 255

RESULT 3
CD40_BOVIN
ID CD40_BOVIN STANDARD; PRT; 269 AA.

AC Q28203;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).
GN TNFRSF5 OR CD40.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=97281252; PubMed=9135560;
RA Hirano A., Brown W.C., Estes D.M.;
RT "Cloning, expression and biological function of the bovine CD40
homologue: role in B-lymphocyte growth and differentiation in
cattle.";
RT Immunology 90:294-300(1997).
RL -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

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DR EMBL: U57745; AAC48710.1; -
DR HSSP: P25942; ICDF.
DR InterPro: IPR001368; -
DR Pfam: PF00020; TNFR_C6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS00650; TNFR_NGFR_2; 1.
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT CHAIN 1 19
FT DOMAIN 20 >269 POTENTIAL.
FT TRANSMEM 194 215 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 187 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 269 269
SQ SEQUENCE 269 AA; 23983 MM; 74690330F95F87 CRC64;

Query Match 16.9%; Score 267; DB 1; Length 269;
Best Local Similarity 28.0%; Pred. No. 7.7e-15;
Matches 65; Conservative 43; Mismatches 110; Indels 14; Gaps 5;

0Y 20 VLRLVLYTLGLG---APCYAPALPSCKEDEYPYGSECCPCSGRYKAEAGELTGTGCE 76
Db 1 MVRPLDCLTWFGEFLTAHVSEPAACEKQYPVNSLCCDCLCPGQKLVNDCFTESKTECQ 60
0Y 77 PCPGTYIAHLNGLSKLQOCQMDPAMGLASNSCTENAVGCGSGHICITQDDGHCA 136
Db 61 SCGKGELTWNREKYCHERRCNPGLGRIGQSEGLTLDITICVGEQHC---TSHTCE 117

0Y 137 ACRAVATSSGQRYQKGTESQDILCONCPGHTS-PNGTLEEQHOTKCSML-VTKAGA 194
Db 118 SCTPHSLCLPFGVQKQIATGLDITVCEPCPLGFFSVSSAFKCHRWTSCEKGLVBOHV 177
0Y 195 GTSSSHWMMWFLSGSLVIVICSTVGLICVKKRRKPRGADVKKVVSQRRQ 246
Db 178 GTNKTDVYCGFGQSMKRTLVIPYTMGVFAVL-----VSACIRNITKKRQ 223

RESULT 4
VT2_SFVKA
ID VT2_SFVKA STANDARD; PRT; 325 AA.

AC P23943;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OS Shope fibroma virus (strain Kasza) (SFV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxID=10272;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=87321103; PubMed=2820128;
RA Upton C., Delange A.M., McFadden G.;
RT "Tumorigenic poxviruses: genomic organization and DNA sequence of the
telomeric region of the Shope fibroma virus genome.";
RT Virology 160:20-30(1987).
RN [2]
RN FUNCTION.
RX MEDLINE=91207415; PubMed=1850261;
RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
McFadden G., Goodwin R.G.;
RT "T2 open reading frame from the Shope fibroma virus encodes a soluble
form of the TNF receptor.";
RT Biochem. Biophys. Res. Commun. 176:335-342(1991).
RL -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

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DR EMBL: M17433; -; NOT_ANNOTATED_CDS.
DR EMBL: A23727; CA01687.1; -
DR PIR: B43692; B43692.
DR HSSP: P19438; ITNR.
DR InterPro: IPR001368; -
DR Pfam: PF00020; TNFR_C6; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00650; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Repeat; Signal.
FT CHAIN 1 16
FT SIGNAL 1 16
FT DOMAIN 17 325 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
FT REPEAT 27 186 4 X TNFR-CYS.
FT REPEAT 63 104 TNFR-CYS 1.
FT REPEAT 105 147 TNFR-CYS 2.
FT REPEAT 148 186 TNFR-CYS 3.
FT REPEAT 181 205 TNFR-CYS 4.
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 325 AA; 35132 MM; 810530339198A71E CRC64;

Query Match 16.5%; Score 260; DB 1; Length 325;
 Best Local Similarity 31.5%; Pred. No. 3.4e-14;
 Matches 62; Conservative 25; Mismatches 80; Indels 30; Gaps 8;

QY 20 VLRVLYLTGLGACVAPALP-----SKEDKPVGSECCPKSPGTRYKACGELTGT 73
 DB 1 MRLRIALLVCV-VYVVDVDPYSSNCGCGHDEKDLGCASCHPFPVARSRLCGPGSNT 59
 OY 74 VCEPCPGPTIAHLNGLSKLCOCMCPAMG-LRASRNCSTENAVCGSGPHFCIYQDG 132
 DB 60 VCSCEGEGTSTAATNNAAPVACVSCR--GPGTGHSESPGCRTHDRVCNCSGTACLLKQ 117
 OY 133 DHCACRAVATSSPGQGVQKGTESODTLQCNCPPGTFSPN-GTLEEC-----179
 DB 118 NGCRIC-APQTKCPAGYGVSGHFRAGDTLCEKCPHTYSDLSPTERCSTSPNYISVGFN 176
 OY 180----QHOKCSMLVTKAG 193
 DB 177 LYPVNETSCT--TTAG 190

RESULT 5
 TNFR_HUMAN
 ID TNFR2_HUMAN STANDARD; PRT; 461 AA.
 AC P20333;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR
 BINDING PROTEIN 2) (TNF1) (P80) (TNF-R2) (CD120b) (ETANERCEPT).
 GN TNFRSF1B OR TNFR2 OR TNFR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90260639; PubMed=2160731;
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
 RA Dower S.K., Cosman D., Goodwin R.G.;
 RT "A receptor for tumor necrosis factor defines an unusual family of
 RT cellular and viral proteins.";
 RL Science 248:1019-1023(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91045991; PubMed=2172983;
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
 RT "A second tumor necrosis factor receptor gene product can shed a
 RT naturally occurring tumor necrosis factor inhibitor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96299745; PubMed=8661109;
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
 RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.;
 RA Brodeur G.M.;
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";
 RL Genomics 33:94-100(1996).
 RN [4]
 RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=90349572; PubMed=216946;
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
 RA Ringold G.M.;
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor
 RT and demonstration of a shed form of the receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
 RN [5]
 RP SEQUENCE OF 27-31.
 RX MEDLINE=90110215; PubMed=2153136;
 RA Engelmann H., Novick D., Wallach D.;
 RT "Two tumor necrosis factor-binding proteins purified from human
 RT urine. Evidence for immunological cross-reactivity with cell surface

RT tumor necrosis factor receptors.";
 RN J. Biol. Chem. 265:1531-1536(1990).
 RN [6]
 RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
 RX MEDLINE=91056048; PubMed=2173696;
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
 RA Brocchhaus M.;
 RT "Purification and partial amino acid sequence analysis of two
 RT distinct tumor necrosis factor receptors from HL60 cells.";
 RL J. Biol. Chem. 265:20131-20138(1990).
 RN [7]
 RP CHARACTERIZATION.
 RX MEDLINE=93016040; PubMed=1328224;
 RA Penica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
 RA Lipari M.T., Goeddel D.V.;
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
 RT Characterization of ligand binding, internalization, and receptor
 RT phosphorylation.";
 RL J. Biol. Chem. 267:21172-21178(1992).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.
 RX MEDLINE=99221490; PubMed=10206649;
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
 RT "Structural basis for self-association and receptor recognition of
 RT human TRAF2.";
 RL Nature 398:533-538(1999).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
 CC LEVEL ON THREONINE RESIDUES.
 CC -1- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND
 CC MYERH-AYERST). USED TO TREAT MODERATE TO SEVERE RHEUMATOID
 CC ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING
 CC PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO
 CC TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm".
 CC -1- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;
 CC WWW="http://www.enbrelinfo.com/".
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 CC -----
 DR EMBL: M32315; AAA59929.1; -
 DR EMBL: M35857; AAA63262.1; -
 DR EMBL: U52165; AAC50622.1; -
 DR EMBL: U52165; AAC50622.1; JOINED.
 DR EMBL: U52157; AAC50622.1; JOINED.
 DR EMBL: U52158; AAC50622.1; JOINED.
 DR EMBL: U52159; AAC50622.1; JOINED.
 DR EMBL: U52160; AAC50622.1; JOINED.
 DR EMBL: U52161; AAC50622.1; JOINED.
 DR EMBL: U52162; AAC50622.1; JOINED.
 DR EMBL: U52163; AAC50622.1; JOINED.
 DR EMBL: U52164; AAC50622.1; JOINED.
 DR EMBL: M55994; AAA6755.1; -
 DR PIR: A35356; A35356.
 DR PIR: A36007; A36007.
 DR PIR: A36475; A36475.
 DR PIR: B35010; B35010.
 DR PIR: A23666; A23666.
 DR PDB: 1CA9; 12-APR-99.
 DR MIM: 191191; -
 DR InterPro: IPR001368; -
 DR Pfam: PF00020; TNFR_c6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.

Query Match	16.4%	Score 259;	DB 1;	Length 461;
Best Local Similarity	32.8%	Pred. No. 5.6e-14;		
Matches	59;	Conservative	23;	Mismatches 76;
			Indels	22;
			Gaps	6;

RESULT	6		
VC22_VARV			
ID	VC22_VARV	STANDARD;	PRT;
	P34015		349 AA

DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE PROTEIN C22/B28 HOMOLOG.
GN GAR.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=INDIA-1967 / ISOLATE IND3;
RX MEDLINE=93202281; Pubmed=8384129;
RA Shchelkunov S.N., Bilinov V.M., Sandakhhchlev L.S.;
RT "genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms.";
RL FEBS Lett. 319:80-83(1993).
CC 1-1 SIMILARITY: COMTAINS 2 LA-NGPR/TNFR-TYPE CYSTEINE-RICH REGIONS.
CC -----
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Query Match	16.3%;	Score 257;	DB 1;	Length 349;
Best Local Similarity	29.3%;	Pred. No. 6, 3e-14;		
Matches 66;	Conservative 23;	Mismatches 94;	Indels 42;	Gaps 8;

RESULT	7	
TNRC_HUMAN		
ID	TNRC_HUMAN	STANDARD;
NC	P36041	PRT; 435 AA

DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR).
DE 2 RELATED PROTEIN (TUMOR NECROSIS FACTOR C RECEPTOR).
GN LTRB OR TNFR OR TNFRSF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A.
RN RP TISSUE=Liver;
RC MEDLINE=93252381; PubMed=8486360;
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human 12p
transcribed sequences derived from a somatic cell hybrid.";
RL Genomics 16:214-218(1993).
[2]
RN FUNCTION.
RP MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., van Arsdele T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfeld B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RL Science 264:707-710(1994).

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CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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CC
CC EMBL: L04270; AAA36757.1; -.
CC HSSP: P25942; ICDF.
CC MIM: 600979; -.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_C6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
KM Receptor: Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 435
FT DOMAIN 31 227
FT TRANSMEM 228 248
FT DOMAIN 249 435
FT DOMAIN 42 211
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 168
FT REPEAT 169 211
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 148
FT DISULFID 142 167
FT DISULFID 170 185
FT CARBOHYD 40 40
FT CARBOHYD 177 177
FT CARBOHYD 177 177
SO SEQUENCE 435 AA; 46709 MW; 624626B6022F656F CRC64;

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RESULT 8
ID TNRC_MOUSE STANDARD; PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
GN LYMR OR TNFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CVB; TISSUE=Lung;
RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression.";
RJ J. Immunol. 155:5280-5288(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9613885; PubMed=8586432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Saayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT sequence trap and chromosomal mapping.";
RJ Genomics 30:312-319(1995).
CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC
CC EMBL: U29173; AA68964.1; -.
CC EMBL: L38423; AAB00846.1; -.
CC EMBL: U30798; AA81334.1; -.
CC HSSP: P25942; ICDF.
CC MGD: MGI:104875; ltblr.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_C6; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
KM Receptor: Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 415
FT DOMAIN 31 223
FT TRANSMEM 224 244
FT DOMAIN 245 415
FT DOMAIN 42 213
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 170
FT REPEAT 171 213
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 150

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FT DISULFID 142 169 BY SIMILARITY.
 FT DISULFID 172 187 BY SIMILARITY.
 FT CARBOHYD 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;

Query Match 15.6%; Score 245.5; DB 1; Length 415;
 Best Local Similarity 25.9%; Pred. No. 6.3e-13;
 Matches 83; Conservative 40; Mismatches 115; Indels 83; Gaps 15;

QY 7 WGP-----PWRSTPRTDYLRLVLYLTFGLGAPCYAPALPSCKEDEV-- 47
 DB 14 WGPLLGLSLVLSQPOLVPPRYENOT-----CWD-----ODKEYE 52
 QY 48 PVGSCPKSPGYRVKACGELGTVCPCPGTYIAHLNGLSKLQCGMCDPAMGARA 107
 DB 53 PMHVCSCRCPPGEFVAVGSRSDTYCKTCHNSYNEHMHSLTQLCRCDIYLFEE 112
 QY 108 SRNCSRTENAVCGSPGHFCIVODGD--HCAACRAVATSSPGORVOKGTESSQ----- 158
 DB 113 VAPCTSDKACRCQPGMCSYVLDNECVHCEERLY-----LCQGTAEATYDELMD 164
 QY 159 -DTLCQNCPPGTF---SPNGTLEBCHQHTKCSML-VTKAGAGTSSSHWV----- 202
 DB 165 TDVNCVPCPKPHFQNTSSPRA---RCQPHTRCEIQGLVEAPGTSYSPDICKNPPPCGAM 221
 QY 203 -WVFLSGLVIVICSTPGLICVKKRRKRDYKVIYSVQRKQDEAGETVIEALQAP 261
 DB 222 LLALILSLVLFETY--LACAMMRHP--SLCKRLGLTLKRHEGE-ESPCCAPAPRAD 276
 QY 262 PDVTVAVETIPSTFGSPN 282
 DB 277 PHFPDLA-EPLLPMSGDLSPS 296

RESULT 9

OX40_RAT STANDARD; PRT; 271 AA.
 AC P15725;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).
 GN TNFRSF4 OR TRXPL1 OR OX40.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=90214614; PubMed=2157591;
 RA Mallett S., Fossum S., Barclay A.N.;
 RT "Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes -- a molecule related to nerve growth factor receptor.";
 RL EMO J. 9:1063-1068(1990).
 CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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 CC EMBL: X17037; CA34897.1; -
 DR PIR: S08036; S08036.
 DR PIR: S12783; S12783.

DR HSSP; P25942; 1CDF.
 DR InterPro: IPR001368; -
 DR Pfam: PF00020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS00050; TNFR_NGFR_2; 2.
 KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;

FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 271 OX40L RECEPTOR.
 FT DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 211 235 POTENTIAL.
 FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 25 164 4 X TNFR-CYS.
 FT REPEAT 25 60 TNFR-CYS 1.
 FT REPEAT 61 102 TNFR-CYS 2.
 FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).
 FT REPEAT 124 164 TNFR-CYS 4.
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;

Query Match 15.2%; Score 240.5; DB 1; Length 271;
 Best Local Similarity 34.9%; Pred. No. 1.1e-12;
 Matches 51; Conservative 16; Mismatches 54; Indels 25; Gaps 5;

QY 41 SCKDEYVVGSECCPKSPGYRVKACGELGTVCPCPGTYIAHLNGLSKLQCGMCD 100
 DB 25 NCVADTYPSGKHCRCRCQPGHGMVSRCDHTDYCHCRPGFYMAVN-YPTQCGQCN 83
 QY 101 PAMGLASRNCSRTENAVCGSPGHFCIVODGDHCAACRAVATSSPGORVOKGTESSDT 160
 DB 84 HRSGSELKQNTPTEDYVQCRPG--TOPRODSSH-----KLQVD----- 121
 QY 161 LCQNCPPGTFSPNGTLEBCHQHTKCS 186
 DB 122 -CVPCPPGHFSP-GSNQACKPWNTCT 145

RESULT 10

VT2_MXVXL STANDARD; PRT; 326 AA.
 AC P29825;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
 GN T2.
 OS Myxoma virus (strain Lausanne).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Leporipoxvirus.
 OX NCBI_TaxID=31530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9135768; PubMed=1651597;
 RA Upton C., Macen J.L., Schreiber M., McFadden G.;
 RT "Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor receptor gene family that contributes to viral virulence.";
 RL Virology 184:370-382(1991).
 CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL ANTI-VIRAL EFFECTS OF THE CYTOKINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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 CC EMBL: M95181; AAA4632.1; -
 DR EMBL: M95181; AAA4632.1; -

DR EMBL: A23729; CAA01688.1; -
 DR PIR: A40566; GOVZML.
 DR HSSP: P19438; 1TNR.
 DR InterPro: IPR001368; -
 DR Pfam: PF00020; TNR_c6; 2.
 DR PROSITE: PS00652; TNR_NGFR_1; 2.
 DR PROSITE: PS50050; TNR_NGFR_2; 2.
 DR Receptor: Glycoprotein; Repeat; Signal.
 DR SIGNAL: 1 16
 FT CHAIN 17 326 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
 FT DOMAIN 27 186 4 X TNR-CYS.
 FT REPEAT 27 62 TNR-CYS 1.
 FT REPEAT 63 104 TNR-CYS 2.
 FT REPEAT 105 147 TNR-CYS 3.
 FT REPEAT 148 186 TNR-CYS 4.
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 326 AA; 35208 MW; ABBF027E947292FF CRC64;

Query Match 15.18; Score 238.5; DB 1; Length 326;
 Best Local Similarity 26.84; Pred. No. 1.9e-12;
 Matches 73; Conservative 30; Mismatches 104; Indels 65; Gaps 11;

QY 20 VLRLVLYTFV-----GAPCYAPALPSCKEDEYVSGCCPKSPGYRVKACGELTGT 73
 DB 1 MFRITLLAVACYGGAP-YGADRGKRCNDYERGLCTSPSPSYASRLCGPSDT 59
 QY 74 VCEPCPGTYIAHLNGLSKLQCG-MCDPAMGLASRNCSTENAVAGCGSGHFCIVODG 132
 DB 60 VCSCKNETFTASTNHPACVSCGRGRC-TGHLSQSQCSDTRDVCDSNGNYCLKQ 117
 QY 133 DHACACRAVATSSGQVQGGTSGDTLQCNCPGFSPN-GLLECG----- 180
 DB 118 EGCRIC-APTKCPAGYVSGHRTGDLCTKCPRTYSDAVSSTECTSSFNYSVEFN 176
 QY 181 ----HOKCSWLVRKGA-----GTSSHWMMVFLSGS 209
 DB 177 LYPNDISCT---TTAOPNEVKTSEFSVILNHTDCDPVFHTETRYTSGSGAGGFTTGM 233
 QY 210 ---LVIVVCSVGLIICVKKRPRGDVYKVI 238
 DB 234 DRYONTKCTMLNIEIRCV-----GDAVRTI 260

RESULT 11

FASL_PIG STANDARD; PRT; 332 AA.

AC 077736;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
 DE (APO-1 ANTIGEN) (CD95).
 OS TNFRSF6 OR APT1 OR FAS.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NC NCBITaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
 RT Expression of apoptosis-associated genes in hibernating and stunned
 RT myocardium of pig.;
 RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
 CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
 CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
 CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
 CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
 CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING

CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
 CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
 CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNR-TYPE CYSTEINE-RICH REGION.
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
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 CC -----
 DR EMBL: A4001202; CAA04596.1; -
 DR InterPro: IPR004488; -
 DR InterPro: IPR001368; -
 DR Pfam: PF00531; death; 1.
 DR PROSITE: PS00652; TNR_NGFR_1; 2.
 DR PROSITE: PS50050; TNR_NGFR_2; 2.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
 DR SIGNAL: 1 16
 FT CHAIN 17 332
 FT DOMAIN 17 175
 FT TRANSMEM 176 192
 FT DOMAIN 193 332
 FT DOMAIN 45 164
 FT REPEAT 45 81
 FT REPEAT 82 125
 FT REPEAT 126 164
 FT DOMAIN 227 311
 FT CARBOHYD 38 38
 FT CARBOHYD 116 116
 SO SEQUENCE 332 AA; 37592 MW; 5B8B03682756BF1B CRC64;

Query Match 15.08; Score 236; DB 1; Length 332;
 Best Local Similarity 27.58; Pred. No. 3e-12;
 Matches 65; Conservative 30; Mismatches 95; Indels 46; Gaps 9;

QY 42 CKDEYVSGCCPKSPGYRVKACGELTGT-VCEPCPGP-TYIAHLNGLSKLQCGMC 99
 DB 46 CPEGHREGQFCQPCPGPKRHADCTSPGAPQCVCSGEGDYTDKNHSSKRCRCVC 105
 QY 100 DPMGLASRNCSTENAVAGCGSGHFCIVQDGDHCAACRAVATSSPGQVQGGTSGSD 159
 DB 106 DGEHGLEVENKTRIQTKRCRKNPFCHNSQCEHCNCP----- 144
 QY 160 TLQCNCPGTFSPNGLEEC--OHOKCSWLVRKAGAGSSSHWMMVFLSGSLVIYVCS 217
 DB 145 TTCE-----HGVLENTPTSNKREVFQSAQS-RSNLMLW---ALLILPVP 190
 QY 218 TVGLIICVKKRPRGDVYVQKROEAGEATVIELQAPPDVTVAVEETI 273
 DB 191 LVYREVKRRCKRKNQKRTITS-----NAF-EVPMKIVDLGKYYITRAEQMKI 239

RESULT 12

OX40_MOUSE STANDARD; PRT; 272 AA.

AC P47741;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).
 GN TNFRSF4 OR TXGP1 OR OX40.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX Ncpi_Taxid=10090,
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=94044750; PubMed=8228223;
RA Calderhead D. M., Buhlmann J.E., Van den Eertwegh A.J.,
RA Claassen E., Noelle R.J., Fell H.;
RT "Cloning of mouse OX40: a T cell activation marker that may mediate
  T-B cell interactions."
RL J. Immunol. 151:5261-5271(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95255413; PubMed=7737295;
RA Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Barclay A.N.;
RT "Gene structure and chromosomal localization of the mouse homologue
  of rat OX40 protein."
RL Eur. J. Immunol. 25:926-930(1995).
CC -!- FUNCTION: RECEPTOR FOR THE OX40/GP34 CYTOKINE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
DR EMBL; Z21674; CAAT9772.1; -.
DR EMBL; X85214; CAAS9476.1; -.
DR HSSP; P25942; ICDF.
DR MGD; MGI:104512; Tnfrsf4.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
  Signal.
FT FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 272 OX40 RECEPTOR.
FT DOMAIN 20 211 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 212 236 POTENTIAL.
FT DOMAIN 237 272 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 165 4 X TNFR-CYS.
FT REPEAT 26 61 TNFR-CYS 1.
FT REPEAT 62 103 TNFR-CYS 2.
FT REPEAT 104 124 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 125 165 TNFR-CYS 4.
FT CARBOHYD 144 144 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CONFLICT 15 15 A -> G (IN REF. 2).
SE SEQUENCE 272 AA; 30153 MW; 06E7BB4156FD08E CRC64;

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[illegible]

RESULT	13			
ID	TNR2_MOUSE	STANDARD:	PRT:	474 AA.
AC	P25119; P97893;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).			
CN	TNFRSF1B OR TNFR2 OR TNFR-2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91187885; PubMed=18493278;			
RA	Lewis M., Tataglia L.A., Lee A., Bennett G.L., Rice G.C.,			
RA	Wong G.H., Chen E.Y., Goeddel D.V.;			
RT	"Cloning and expression of cDNAs for two distinct murine tumor			
RT	necrosis factor receptors demonstrate one receptor is species			
RT	specific."			
RL	Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91246168; PubMed=1645445;			
RA	Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,			
RA	Copeland N.G., Jenkins N.A., Smith C.A.;			
RT	"Molecular cloning and expression of the type 1 and type 2 murine			
RT	receptors for tumor necrosis factor";			
RL	Mol. Cell. Biol. 11:3020-3026(1991).			
RN	[3]			
RP	SEQUENCE OF 1-26 FROM N.A.			
RC	STRAIN=NOD.			
RA	Jacob C.O., Liu J.;			
RL	submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE OF 1-22 FROM N.A.			
RC	TISSUE=Liver.			
RA	Kissomergis M., Fellows R., Feldmann M., Chernajovsky Y.;			
RL	submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: RECEPTOR FOR TNF-ALPHA.			
CC	-1- SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; M60469; AAA39752.1; -			
DR	EMBL; M59378; AAA40463.1; -			
DR	EMBL; U39488; AA85021.1; -			
DR	EMBL; X87128; CAA60618.1; -			
DR	PIR; B38634; B38634.			
DR	HSSP; P19438; INCF.			
DR	MGI; MGI:1314883; Tnfisflb.			
DR	InterPro; IPR001368; -			
DR	Pfam; PF00020; TNFR_C6; 4.			
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.			
DR	PROSITE; PS00505; TNFR_NGFR_2; 3.			
KW	Receptor; Transmembrane; Glycoprotein; Repeat; Signal.			
FT	SIGNAL	1	22	
FT	CHAIN	23	474	TUMOR NECROSIS FACTOR RECEPTOR 2.
FT	DOMAIN	23	258	INTRACELLULAR (POTENTIAL).
FT	TRANSMEM	259	288	POTENTIAL.
FT	DOMAIN	289	474	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	39	203	4 X TNFR-CYS.
FT	REPEAT	39	77	TNFR-CYS 1.
FT	REPEAT	78	119	TNFR-CYS 2.
FT	REPEAT	120	164	TNFR-CYS 3.

DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE (APO-1 ANTIGEN) (CD95).
GN TNFRSF6 OR PT1 OR FAS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclerognathia; Muridae; Murinae; Rattus
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=94128114; PubMed=750766;
RA Kimura K., Yamamoto M., Wakatsuki T.;
RT "A variant mRNA species encoding a truncated form of Fas antigen in
RT the rat liver.";
RT Blochm. Biophys. Res. Commun. 198;666-674(1994).
CC -I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -I- SIMILARITY: CONTAINS A LA-NER/TNFR-TYPE CYSTEINE-RICH REGION.
CC -I- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

ID	MSL1_HUMAN	STANDARD;	PRT; 417 AA
AC	Q93038; Q93036; Q93037; Q92983; P78515; Q99831; Q99722; P78507;		
CC	Q99830;		
DC	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DF	01-OCT-2000 (Rel. 40, Last annotation update)		
DE	WSL-1 PROTEIN PRECURSOR (APOPTOSIS-MEDIATING RECEPTOR DR3) (APOPTOSIS-MEDIATING RECEPTOR TRAMP) (DEATH DOMAIN RECEPTOR 3) (WSL PROTEIN)		
DE	(APOPTOSIS INDUCING RECEPTOR AIR) (APO-3) (LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH) (LARD).		
GN	TNFRSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DDR3.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
NN	[1]		

RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS.
 RC TISSUE=Lymphoid;
 RX MEDLINE=97088617; Pubmed-89345425;
 RA Kitchin J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,
 RA Grlinham G.J., Brown R., Farrow S.N.;
 RT "A death-domain-containing receptor that mediates apoptosis.";
 RL Nature 384:372-375(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=umbilical vein endothelial cells;
 RX MEDLINE=97081063; Pubmed-8875942;
 RA Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,
 RA Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;
 RT "Signal transduction by DR3, a death domain-containing receptor
 RT related to TNFR-1 and CD95.";
 RL Science 274:990-992(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=97148200; Pubmed-86994832;
 RA Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,
 RA Goddard A.D., Bauer K.D., Ashkenazi A.;
 RT "Apo-3, a new member of the tumor necrosis factor receptor family,
 RT contains a death domain and activates apoptosis and NF-kappa-B";
 RL Curr. Biol. 6:1669-1676(1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97272273; Pubmed-9114039;
 RA Screaton G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,
 RA McMichael A.J., Bell J.I.;
 RT "LARD: a new lymphoid-specific death domain containing receptor
 RT regulated by alternative pre-mRNA splicing.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
 RN [6]
 RP SEQUENCE OF 4-417 FROM N.A.
 RC TISSUE=Brain, and Fetal lung;
 RX MEDLINE=97205335; Pubmed-9052839;
 RA Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
 RA Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E.,
 RA Browning J.R., MacDonald H.R., Tschoopp J.;
 RT "FRAP, a novel apoptosis-mediating receptor with sequence homology
 RT to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
 RL Immunity 6:79-86(1997).
 RN [7]
 RP SEQUENCE OF 7-417 FROM N.A.
 RC TISSUE=Brain;
 RA Chaudhary P.M., Hood L.E.;
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
 CC -I- FUNCTION: INDUCES APOPTOSIS AND ACTIVATES NUCLEAR FACTOR KAPPA-B
 CC (NF-KAPPA-B). DIRECTLY INTERACTS WITH TRADD ADAPTOR MOLECULE. MAY
 CC PLAY A ROLE IN REGULATING LYMPHOCYTE HOMEOSTASIS.
 CC -I- SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH
 CC THE TNFR1-ASSOCIATED MOLECULE TRADD AND THE TNFR1 RECEPTOR TO
 CC ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING.
 CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
 CC -I- ALTERNATIVE PRODUCTS: 3 ISOFORMS: WSL-1/LARD-1A (SHOWN HERE),
 CC WSL-ST/LARD-3 AND WSL-52; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -I- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND
 CC LYMPHOCYTES. DETECTED IN LYMPHOIC TISSUES SUCH AS THYMUS,
 CC COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.
 CC -I- PIM: GLYCOSYLATED (PROBABLE).
 CC -I- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -I- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

CC	entitled and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).					
CC						
CC						
DR	EMBL:	Y09392:	CAA70561.1;	-	-	POTENTIAL.
DR	EMBL:	Y09392:	CAA70559.1;	-	-	WSL-1 PROTEIN.
DR	EMBL:	Y09392:	CAA70560.1;	-	-	EXTRACELLULAR (POTENTIAL).
DR	EMBL:	U72763:	AAC50819.1;	-	-	POTENTIAL.
DR	EMBL:	U83599:	AAB41434.1;	-	-	CYTOSOLASMIC (POTENTIAL).
DR	EMBL:	U83600:	AAB41435.1;	-	-	4 X TNFR-CYS.
DR	EMBL:	U78029:	AAB40918.1;	-	-	TNFR-CYS 1.
DR	EMBL:	U74611:	AAB39714.1;	-	-	TNFR-CYS 2.
DR	EMBL:	U94501:	AAC51306.1;	-	-	TNFR-CYS 3.
DR	EMBL:	U94504:	AAC51309.1;	-	-	TNFR-CYS 4.
DR	EMBL:	U75380:	AAC51192.1;	-	-	DEATH DOMAIN.
DR	EMBL:	U75381:	AAC51193.1;	-	-	N-LINKED (GLCNAC. . .) (POTENTIAL).
DR	EMBL:	U83597:	AAB41432.1;	-	-	N-LINKED (GLCNAC. . .) (POTENTIAL).
DR	HSSP:	P19438:	ITNR.	-	-	STLCSPERCAVCGMROMFVOVLALAVPLLIGA ->
DR	MIM:	603366:	ITNR.	-	-	VLGAPGPMGCPPIAMGHPLHLPPLIASQAGVCR (IN
DR	InterPro:	IPR000468:	-	-	-	ISOFORM WSL-S1).
DR	InterPro:	IPR001368:	-	-	-	MISSING (IN ISOFORM WSL-S1).
DR	Pfam:	PF00020:	TNFR_C6; 2.	-	-	MEMVOVLLAGLVPLLLGATLTYYTHCWHKPLVTADAG
DR	Pfam:	PF00531:	death; 1.	-	-	MEALTPPATHTLS -> SRMGAGNARGTGMDSRGAGEGG
DR	PROSITE:	PS00652:	TNFR_NGFR_1; 2.	-	-	NHPTPTSCFGSGSRCSWIALMLSPCLGP (IN
DR	PROSITE:	PS00500:	TNFR_NGFR_2; 1.	-	-	ISOFORM WSL-S2).
DR	PROSITE:	PS50017:	DEATH_DOMAIN; 1.	-	-	MISSING (IN ISOFORM WSL-S2).
KW	Receptor;	Apoptosis;	Alternative splicing;	Transmembrane;	Signal;	L->A: SUPPRESSES HOMODIMERIZATION, TNFR1
KW	Repeat.					INTERACTION, AND APOPTOSIS INDUCTION.
FT	SIGNAL	1	24			L->B: SUPPRESSES HOMODIMERIZATION, AND
FT	CHAIN	25	417			TNFR1 INTERACTION.
FT	DOMAIN	25	199			D->A: SUPPRESSES HOMODIMERIZATION, AND
FT	TRANSLEM	200	220			TNFR1 INTERACTION.
FT	DOMAIN	223	417			RPR -> AAA (IN REF. 6).
FT	DOMAIN	34	192			P -> H (IN REF. 7).
FT	REPEAT	34	71			P -> L (IN REF. 6 AND 7).
FT	REPEAT	72	115			A -> R (IN REF. 1).
FT	REPEAT	116	163			R -> L (IN REF. 1).
FT	REPEAT	164	192			R -> H (IN REF. 1).
FT	DOMAIN	332	413			5226319DDBA6706 CXC64;
FT	CARBOHYD	67	67			
FT	CARBOHYD	106	106			
FT	VARSPLIC	182	218			
FT						
FT	VARSPLIC	219	417			
FT	VARSPLIC	200	253			
FT						
FT	VARSPLIC	254	417			
FT	MUTAGEN	354	354			
FT	MUTAGEN	356	356			
FT	MUTAGEN	373	373			
FT	CONFLICT	4	6			
FT	CONFLICT	167	167			
FT	CONFLICT	312	312			
FT	CONFLICT	370	370			
FT	CONFLICT	381	381			
SO	SEQUENCE	417 AA;	45385 MW;			

Query Match 13.1%; Score 206.5; DB 1; Length 417;
 Best Local Similarity 27.4%; Pred. No. 9.1e-10;
 Matches 74; Conservative 28; Mismatches 119; Indels 49; Gaps 13;

25 LYRLFGLARPCY-----APALPGCKDEDIEFYVGSSCCCKSGPYVKAKCEELNG-TVCPECP 79
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 15 LLIVLLVLRRAAGGTSTRPCDCAGDHKKRTIGLECCGCGRGHTLKARPCTEPCGNSTCVLCP 74

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Search completed: April 25, 2001, 17:36:13
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